(1) GENERAL INFORMATION:

- (i) APPLICANTS: Boon, Thierry, Van den Eynde, Benoît
- (ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor Rejection Antigens and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Felfe & Lynch
 - (B) STREET: 805 Third Avenue
 - (C) CITY: New York City
 - (D) STATE: New York
 - (F) ZIP: 10022
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 - (B) COMPUTER: IBM
 - (C) OPERATING SYSTEM: PC-DOS
 - (D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/807,043
 - (B) FILING DATE: 12-DECEMBER-1991
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/764,364
 - (B) FILING DATE: 23-SEPTEMBER-1991
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/728,838
 - (b) FILING DATE: 9-JULY-1991
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/705,702
 - (B) FILING DATE: 23-May-1991
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hanson, Norman D.
 - (B) REGISTRATION NUMBER: 30,946
 - (C) REFERENCE/DOCKET NUMBER: LUD 253.3
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 688-9200
 - (B) TELEFAX: (212) 838-3884

- (2) INFORMATION FOR SEQUENCE ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACCACAGGAG	AATGAAAAGA	ACCCGGGACT	CCCAAAGACG	CTAGATGTGT	GAAGATCCTG	60
ATCACTCATT	GGGTGTCTGA	GTTCTGCGAT	ATTCATCCCT	CAGCCAATGA	GCTTACTGTT	120
CTCGTGGGGG	GTTTGTGAGC	CTTGGGTAGG	AAGTTTTGCA	AGTTCCGCCT	ACAGCTCTAG	180
CTTGTGAATT	TGTACCCTTT	CACGTAAAAA	AGTAGTCCAG	AGTTTACTAC	ACCCTCCCTC	240
CCCCCTCCCA	CCTCGTGCTG	TGCTGAGTTT	AGAAGTCTTC	CTTATAGAAG	TCTTCCGTAT	300
AGAACTCTTC	CGGAGGAAGG	AGGGAGGACC	CCCCCCTTT	GCTCTCCCAG	CATGCATTGT	360
GTCAACGCCA	TTGCACTGAG	CTGGTCGAAG	AAGTAAGCCG	CTAGCTTGCG	ACTCTACTCT	420
TATCTTAACT	TAGCTCGGCT	TCCTGCTGGT	ACCCTTTGTG	CC		462

(2)		I) I)		CE CHENGTHE PER POLICE	HARACH: (Control of the control of t	TERI 575 l cleio lin	STIC pase c ac: near	cs: pain id	cs							
	(x:	i) S1	EQUE	VCE I	DESC	RIPT	ON:	SE	Q ID	NO:	2:					
		GAT Asp														4.8
		GAT Asp														96
		CTG Leu 35														144
		CTG Leu														192
		AGG Arg														240
		GAT Asp														288
GAC Asp	GAC Asp	GAG Glu	GAC Asp 100	GAC Asp	GAC Asp	GAC Asp	GAT Asp	GCC Ala 105	TTC Phe	TAT Tyr	GAT Asp	GAT Asp	GAG Glu 110	GAT Asp	GAT Asp	336
GAG Glu	GAA Glu	GAA Glu 115	GAA Glu	TTG Leu	GAG Glu	AAC Asn	CTG Leu 120	ATG Met	GAT Asp	GAT Asp	GAA Glu	TCA Ser 125	GAA Glu	GAT Asp	GAG Glu	384
GCC Ala	GAA Glu 130	GAA Glu	GAG Glu	ATG Met	AGC Ser	GTG Val 135	GAA Glu	ATG Met	GGT Gly	GCC Ala	GGA Gly 140	GCT Ala	GAG Glu	GAA Glu	ATG Met	432
GGT Gly 145	GCT Ala	GGC Gly	GCT Ala	AAC Asn	TGT Cys 150	GCC Ala	TGT Cys	GTT Val	CCT Pro	GGC Gly 155	CAT His	CAT His	TTA Leu	AGG Arg	AAG Lys 160	480
AAT Asn	GAA Glu	GTG Val	AAG Lys	TGT Cys 165	AGG Arg	ATG Met	ATT Ile	TAT Tyr	TTC Phe 170	TTC Phe	CAC His	GAC Asp	CCT Pro	AAT Asn 175	TTC Phe	528

			AAC Asn					576
	 	 	 GTT Val	 	 	 	 	 624
		Glu	GAA Glu					672
TAG								675

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(2)	INFORMATION	FOR	SEQUENCE	ID NO:	3:
	(i) SEQUENCE	CHI	PACTEDIC	PTCG.	

- (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 228 base pairs

 (B) TYPE: nucleic acid

 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: genomic DNA

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCATGCAGTT	GCAAAGCCCA	GAAGAAAGAA	ATGGACAGCG	GAAGAAGTGG	TTGTTTTTTT	60
TTCCCCTTCA	TTAATTTTCT	AGTTTTTAGT	AATCCAGAAA	ATTTGATTTT	GTTCTAAAGT	120
TCATTATGCA	AAGATGTCAC	CAACAGACTT	CTGACTGCAT	GGTGAACTTT	CATATGATAC	180
ATAGGATTAC	ACTTGTACCT	GTTAAAAATA	AAAGTTTGAC	TTGCATAC		228

- (2) INFORMATION FOR SEQUENCE ID NO: 4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1365 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT	50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT	100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG	150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT	200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA	250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT	300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG	350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG	400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT	450
ACCCTTTGTG CC	462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA	504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG	546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
GAT GAA GAC GAT GAG GAT GAG GAT GAC TAC TAC GAC GAC	756
GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	798
GAG GAA GAA TTG GAG AAC CTG ATG GAT GAA TCA GAA	840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT	924
GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG AT	966
TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG	1008
AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT	1050
GAA GAG GTT GCA ATG GAA GAA GAA GAA GAA GAG GAG	1092
GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT	1134
TAG	1137
GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG	1187
TTGTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA	1237
ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT	1287
CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT	1337
GTTAAAAATA AAAGTTTGAC TTGCATAC	1365

- INFORMATION FOR SEQUENCE ID NO: 5: (2)
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4698 base pairs
 (B) TYPE: nucleic acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

1001010101011011110111101111011		
ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG		50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT		100
	CTTGGGTAGG	150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT		200
	CCCCTCCCA	250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG	TCTTCCGTAT	300
	GCTCTCCCAG	350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG	AAGTAAGCCG	400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT	TCCTGCTGGT	450
ACCCTTTGTG CC		462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC	AGT GGC TCA	504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA		546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG		588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC		630
	GAT GTG GCC	672
	GTC GAT GAG	714
GAT GAA GAC GAT GAG GAT GAG GAT GAC TAC		756
	GAG GAT GAT	798
	GAA TCA GAA	840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG		882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC	T	916
GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT		966
	GGGTCATTGC	1016
TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC		
CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG	-	1066
TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC		1116
TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT	CTTGCTCCCC	1166
THE CLEAR CONTRACTOR OF THE CO	CCCCACCCTC	1216
	TTCCTGTTCC	1266
	TATTTACCTT	1316
TO COMPANY OF THE PARTY OF THE	CCTTTTCTTT	1366
The state of the s	CGCTTTTCCT	1416
The state of the s	CATTTTCGGG	1466
COMPAGE CONTROL CONTRO	TTCGGGTGCT	1516
CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT	TTTTTTTTT	1566
TTGGTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTGGCT	GTCCTGGCAC	1616
TCACTCTGTA GACCAGGCTG GCCTCAAACT CAGAAATCTG	CCTGCCTCTG	1666
CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC	CCCAGTGCAG	1716
GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT	TCTGCATGTT	1766
AACTCCCCTT TTGGCACCTT TCCTTTACAG GACCCCCTCC	CCCTCCCTGT	1816
TTCCCTTCCG GCACCCTTCC TAGCCCTGCT CTGTTCCCTC	TCCCTGCTCC	1866
CCTCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC	CCTGCTTTCT	1916
GCCCCGTTCC CCTTTTTTGT GCCTTTCCTC CTGGCTCCCC	TCCACCTTCC	1966
AGCTCACCTT TTTGTTTGTT TGGTTGTTTG GTTGTTTGGT	TTGCTTTTTT	2016

TTTTTTTTT GCACCTTGTT TTCCAAGATC CCCCTCCCCC TCCGGCTTC	
CCTCTGTGTG CCTTTCCTGT TCCCTCCCC TCGCTGGCTC CCCCTCCCT	T 2116
TCTGCCTTC CTGTCCCTGC TCCCTTCTCT GCTAACCTTT TAATGCCTT	T 2166
CTTTTCTAGA CTCCCCCCTC CAGGCTTGCT GTTTGCTTCT GTGCACTTT	T 2216
CCTGACCCTG CTCCCCTTCC CCTCCCAGCT CCCCCCTCTT TTCCCACCT	C 2266
CCTTTCTCCA GCCTGTCACC CCTCCTTCTC TCCTCTGT TTCTCCCAC	T 2316
TCCTGCTTCC TTTACCCCTT CCCTCTCCCT ACTCTCCTCC CTGCCTGCT	G 2366
GACTTCCTCT CCAGCCGCCC AGTTCCCTGC AGTCCTGGAG TCTTTCCTG	C 2416
CTCTCTGTCC ATCACTTCCC CCTAGTTTCA CTTCCCTTTC ACTCTCCCC	
ATGTGTCTCT CTTCCTATCT ATCCCTTCCT TTCTGTCCCC TCTCCTCTG	
CCATCACCTC TCTCCTCCCT TCCCTTTCCT CTCTCTTCCA TTTTCTTCC	
CCTGCTTCTT TACCCTGCCT CTCCCATTGC CCTCTTACCT TTATGCCCA	
TCCATGTCCC CTCTCAATTC CCTGTCCCAT TGTGCTCCCT CACATCTTC	
ATTTCCCTCT TTCTCCCTTA GCCTCTTCTT CCTCTTCTCT TGTATCTCC	
TTCCCTTTGC TTCTCCCTCC TCCTTTCCCC TTCCCCTATG CCCTCTACT	
TACTTGATCT TCTCTCCTCT CCACATACCC TTTTTCCTTT CCACCCTGC	
CTTTGTCCCC AGACCCTACA GTATCCTGTG CACAGGAAGT GGGAGGTGC	
ATCAACAACA AGGAGGCAAG AAACAGAGCA AAATCCCAAA ATCAGCAGG	
AAGGCTGGAT GAAAATAAGG CCAGGTTCTG AGGACAGCTG GAATCTAGC	
AAGTGGCTCC TATAACCCTA AGTACCAAGG GAGAAAGTGA TGGTGAAGT	
CTTGATCCTT GCTGCTTCTT TTACATATGT TGGCACATCT TTCTCAAAT	
CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA AGTAATGGG	
GAATCTGAAA ACTAGGGGCC AGTGGTTTGT TTTGGGGACA AATTAGCAC	
TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA TGATTTGAG	
TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA GTTCTTTTT	
GGCTAAAGAT ACTTGGAACC ATAGAAGCGT TGTTAAAATA CTGCTTTCT	
TTGCTAAAAT ATTCTTTCTC ACATATTCAT ATTCTCCAG	· -
GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG T	3355
AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT G	CT 3438
AAT GCT GAT GAA GAG GTT GCA ATG GAA GAA GAA GAA GAA GAA	
GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT G TTC TCA CCT TAG	
	3576
GCATGCAGGT ACTGGCTTCA CTAACCAACC ATTCCTAACA TATGCCTGT	
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTT	
TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGA	
CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGAT	
GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAG	
GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATT	
TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTG	
TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTC	
TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATC	
CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCAC	
TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTTA GATTTCTTA	
AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAG	
GTAACTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGG	
GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTG	
CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAAT	C 4326
ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAA	
	T 4376
ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGA	T 4376
	T 4376 A 4426
ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGA	T 4376 A 4426 C 4476
ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGA AGTCAGGAGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT TTTCTTCTA AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTT	T 4376 A 4426 C 4476 T 4526
ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGA AGTCAGGAGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT TTTCTTCTA	T 4376 A 4426 C 4476 T 4526 A 4576

GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA AATAAAAGTT TGACTTGCAT AC

- (2) INFORMATION FOR SEQUENCE ID NO: 6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu

- (2) INFORMATION FOR SEQUENCE ID NO: 7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2418 base pairs
 - (B) TYPE: nucleic acid (D) TOPOLOGY: linear

 - (ii) MOLECULE TYPE: genomic DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCAGGC	CCTGCCAGGA	AAAATATAAG	GGCCCTGCGT	GAGAACAGAG	50
GGGGTCATCC	ACTGCATGAG	AGTGGGGATG	TCACAGAGTC	CAGCCCACCC	100
TCCTGGTAGC	ACTGAGAAGC	CAGGGCTGTG	CTTGCGGTCT	GCACCCTGAG	150
GGCCCGTGGA	TTCCTCTTCC	TGGAGCTCCA	GGAACCAGGC	AGTGAGGCCT	200
TGGTCTGAGA	CAGTATCCTC	AGGTCACAGA	GCAGAGGATG	CACAGGGTGT	250
GCCAGCAGTG	AATGTTTGCC	CTGAATGCAC	ACCAAGGGCC	CCACCTGCCA	300
CAGGACACAT	AGGACTCCAC	AGAGTCTGGC	CTCACCTCCC	TACTGTCAGT	350
CCTGTAGAAT	CGACCTCTGC	TGGCCGGCTG	TACCCTGAGT	ACCCTCTCAC	400
TTCCTCCTTC	AGGTTTTCAG	GGGACAGGCC	AACCCAGAGG	ACAGGATTCC	450
CTGGAGGCCA	CAGAGGAGCA	CCAAGGAGAA	GATCTGTAAG	TAGGCCTTTG	500
TTAGAGTCTC	CAAGGTTCAG	- +	AGGCCTCTCA	CACACTCCCT	550
CTCTCCCCAG	GCCTGTGGGT	CTTCATTGCC	CAGCTCCTGC	CCACACTCCT	600
GCCTGCTGCC	CTGACGAGAG	TCATCATGTC	TCTTGAGCAG	AGGAGTCTGC	650
ACTGCAAGCC	TGAGGAAGCC	CTTGAGGCCC	AACAAGAGGC	CCTGGGCCTG	700
GTGTGTGTGC	AGGCTGCCAC	CTCCTCCTCC	TCTCCTCTGG	TCCTGGGCAC	750
CCTGGAGGAG	GTGCCCACTG	CTGGGTCAAC	AGATCCTCCC	CAGAGTCCTC	800
AGGGAGCCTC	CGCCTTTCCC	ACTACCATCA	ACTTCACTCG	ACAGAGGCAA	850
CCCAGTGAGG	GTTCCAGCAG	CCGTGAAGAG	GAGGGGCCAA	GCACCTCTTG	900
TATCCTGGAG	TCCTTGTTCC	GAGCAGTAAT	CACTAAGAAG	GTGGCTGATT	950
TGGTTGGTTT	TCTGCTCCTC	AAATATCGAG	CCAGGGAGCC	AGTCACAAAG	1000
GCAGAAATGC	TGGAGAGTGT	CATCAAAAAT	TACAAGCACT	GTTTTCCTGA	1050
	AAAGCCTCTG	AGTCCTTGCA	GCTGGTCTTT	GGCATTGACG	1100
TGAAGGAAGC	AGACCCCACC	-	ATGTCCTTGT	CACCTGCCTA	1150
GGTCTCTCCT	ATGATGGCCT	GCTGGGTGAT	AATCAGATCA	TGCCCAAGAC	1200
AGGCTTCCTG	ATAATTGTCC	TGGTCATGAT	TGCAATGGAG	GGCGGCCATG	1250
CTCCTGAGGA	GGAAATCTGG			GGTGTATGAT	1300
GGGAGGGAGC	ACAGTGCCTA			TCACCCAAGA	1350
TTTGGTGCAG	GAAAAGTACC	TGGAGTACGG	CAGGTGCCGG	ACAGTGATCC	1400
CGCACGCTAT	GAGTTCCTGT	GGGGTCCAAG	GGCCCTCGCT	GAAACCAGCT	1450
ATGTGAAAGT	CCTTGAGTAT	GTGATCAAGG	TCAGTGCAAG	AGTTCGCTTT	1500
TTCTTCCCAT			AGAGAGGAGG	AAGAGGGAGT	1550
CTGAGCATGA	GTTGCAGCCA		GAGGGGGACT	GGGCCAGTGC	1600
ACCTTCCAGG	GCCGCGTCCA	GCAGCTTCCC	CTGCCTCGTG	TGACATGAGG	1650
CCCATTCTTC	ACTCTGAAGA		TGTTCTCAGT	AGTAGGTTTC	1700
TGTTCTATTG	GGTGACTTGG		TTGTTCTCTT	TTGGAATTGT	1750
TCAAATGTTT	TTTTTTAAGG	GATGGTTGAA	TGAACTTCAG	CATCCAAGTT	1800
TATGAATGAC	AGCAGTCACA	CAGTTCTGTG	TATATAGTTT	AAGGGTAAGA	1850
GTCTTGTGTT	TTATTCAGAT	TGGGAAATCC		GTGAATTGGG	1900
ATAATAACAG	CAGTGGAATA		AATGTGAAAA	ATGAGCAGTA	1950
AAATAGATGA	GATAAAGAAC	TAAAGAAATT	AAGAGATAGT	CAATTCTTGC	2000
CTTATACCTC		GTAAAATTTT	TAAAGATATA	TGCATACCTG	2050
GATTTCCTTG	GCTTCTTTGA	GAATGTAAGA	GAAATTAAAT	CTGAATAAAG	2100

AATTCTTCCT	GTTCACTGGC	TCTTTTCTTC	TCCATGCACT	GAGCATCTGC	2150
TTTTTGGAAG	GCCCTGGGTT	AGTAGTGGAG	ATGCTAAGGT	AAGCCAGACT	2200
CATACCCACC	CATAGGGTCG	TAGAGTCTAG	GAGCTGCAGT	CACGTAATCG	2250
AGGTGGCAAG	ATGTCCTCTA	AAGATGTAGG	GAAAAGTGAG	AGAGGGGTGA	2300
GGGTGTGGGG	CTCCGGGTGA	GAGTGGTGGA	GTGTCAATGC	CCTGAGCTGG	2350
GGCATTTTGG	GCTTTGGGAA	ACTGCAGTTC	CTTCTGGGGG	AGCTGATTGT	2400
AATGATCTTG	GGTGGATCC				2418

(2) INFORMATION FOR SEQUENCE ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5724 base pairs

(B) TYPE: nucleic acid (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-1 gene (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

	CACTGGCATC				50
	ATCCAAACAT				100
	TCCACCCCTG				150
	ACTGACTTGA				200
	GGCGGCTTGA				250
	AGGTGACATG				300
	CCCCAAATAA				350
	TCAGGCTGGG				400
CTGGGGACTC	GAAGTCAGAG	CTCCGTGTGA	TCAGGGAAGG	GCTGCTTAGG	450
AGAGGGCAGC	GTCCAGGCTC	TGCCAGACAT	CATGCTCAGG	ATTCTCAAGG	500
AGGGCTGAGG	GTCCCTAAGA	CCCCACTCCC	GTGACCCAAC	CCCCACTCCA	550
	CCGTGACCCA				600
	CCCACCCCAT				650
	CACCCCACC				700
	CCGGTTCCCG				750
	TGCGCATTGT				800
	TAGAGTTCGG				850
	AGAGGCTGAG				900
GAGAGCCCCA	AATATTCCAG	CCCCGCCCTT	GCTGCCAGCC	CTGGCCCACC	950
CGCGGGAAGA	CGTCTCAGCC	TGGGCTGCCC	CCAGACCCCT	GCTCCAAAAG	1000
CCTTGAGAGA	CACCAGGTTC	TTCTCCCCAA	GCTCTGGAAT	CAGAGGTTGC	1050
TGTGACCAGG	GCAGGACTGG	TTAGGAGAGG	GCAGGGCACA	GGCTCTGCCA	1100
GGCATCAAGA	TCAGCACCCA	AGAGGGAGGG	CTGTGGGCCC	CCAAGACTGC	1150
ACTCCAATCC	CCACTCCCAC	CCCATTCGCA	TTCCCATTCC	CCACCCAACC	1200
CCCATCTCCT	CAGCTACACC	TCCACCCCA	TCCCTACTCC	TACTCCGTCA	1250
CCTGACCACC	ACCCTCCAGC	CCCAGCACCA	GCCCCAACCC	TTCTGCCACC	1300
TCACCCTCAC	TGCCCCCAAC	CCCACCCTCA	TCTCTCTCAT	GTGCCCCACT	1350
CCCATCGCCT	CCCCCATTCT	GGCAGAATCC	GGTTTGCCCC	TGCTCTCAAC	1400
CCAGGGAAGC	CCTGGTAGGC	CCGATGTGAA	ACCACTGACT	TGAACCTCAC	1450
AGATCTGAGA	GAAGCCAGGT	TCATTTAATG	GTTCTGAGGG	GCGGCTTGAG	1500
	GGGAGTGGTT				1550
CTGAGGGAGG	ACTGAGGAGG	CACACACCCC	AGGTAGATGG	CCCCAAAATG	1600
ATCCAGTACC	ACCCCTGCTG	CCAGCCCTGG	ACCACCGGC	CAGGACAGAT	1650
GTCTCAGCTG	GACCACCCC	CGTCCCGTCC	CACTGCCACT	TAACCCACAG	1700
GGCAATCTGT	AGTCATAGCT	TATGTGACCG	GGGCAGGGTT	GGTCAGGAGA	1750
GGCAGGGCCC	AGGCATCAAG	GTCCAGCATC	CGCCCGGCAT	TAGGGTCAGG	1800
ACCCTGGGAG	GGAACTGAGG	GTTCCCCACC	CACACCTGTC	TCCTCATCTC	1850
CACCGCCACC	CCACTCACAT	TCCCATACCT	ACCCCCTACC	CCCAACCTCA	1900
TCTTGTCAGA	ATCCCTGCTG	TCAACCCACG	GAAGCCACGG	GAATGGCGGC	1950
CAGGCACTCG	GATCTTGACG	TCCCCATCCA	GGGTCTGATG	GAGGGAAGGG	2000
GCTTGAACAG	GGCCTCAGGG	GAGCAGAGGG	AGGGCCCTAC	TGCGAGATGA	2050

GGGAGGCCTC AGAGGACCCA GCACCCTAGG ACACCGCACC		2100
ACTGAGGCTG CCACTTCTGG CCTCAAGAAT CAGAACGATG		2150
TTGCATGGGG GTGGGACCCA GGCCTGCAAG GCTTACGCGG	AGGAAGAGA	2200
GGGAGGACTC AGGGGACCTT GGAATCCAGA TCAGTGTGGA	CCTCGGCCCT	2250
GAGAGGTCCA GGGCACGGTG GCCACATATG GCCCATATTT	CCTGCATCTT	2300
TGAGGTGACA GGACAGAGCT GTGGTCTGAG AAGTGGGGCC	TCAGGTCAAC	2350
AGAGGGAGGA GTTCCAGGAT CCATATGGCC CAAGATGTGC	CCCCTTCATG	2400
AGGACTGGGG ATATCCCCGG CTCAGAAAGA AGGGACTCCA	CACAGTCTGG	2450
CTGTCCCCTT TTAGTAGCTC TAGGGGGACC AGATCAGGGA	TGGCGGTATG	2500
TTCCATTCTC ACTTGTACCA CAGGCAGGAA GTTGGGGGGC	CCTCAGGGAG	2550
ATGGGGTCTT GGGGTAAAGG GGGGATGTCT ACTCATGTCA	GGGAATTGGG	2600
GGTTGAGGAA GCACAGGCGC TGGCAGGAAT AAAGATGAGT	GAGACAGACA	2650
AGGCTATTGG AATCCACACC CCAGAACCAA AGGGGTCAGC	CCTGGACACC	2700
TCACCCAGGA TGTGGCTTCT TTTTCACTCC TGTTTCCAGA	TCTGGGGCAG	2750
GTGAGGACCT CATTCTCAGA GGGTGACTCA GGTCAACGTA	GGGACCCCCA	2800
TCTGGTCTAA AGACAGAGCG GTCCCAGGAT CTGCCATGCG	TTCGGGTGAG	2850
GAACATGAGG GAGGACTGAG GGTACCCCAG GACCAGAACA		2900
CTGCACAGAA ATCAGCCCTG CCCCTGCTGT CACCCCAGAG		2950
GGGCCGTCTG CCGAGGTCCT TCCGTTATCC TGGGATCATT		3000
ACGGGGAGGC CTTGGTCTGA GAAGGCTGCG CTCAGGTCAG		3050
GTCCCAGGCC CTGCCAGGAG TCAAGGTGAG GACCAAGCGG		3150
CAGGACACAT TAATTCCAAT GAATTTTGAT ATCTCTTGCT		3200
AAGGACCTAG GCACGTGTGG CCAGATGTTT GTCCCCTCCT		3250
TCCTTATCAT GGATGTGAAC TCTTGATTTG GATTTCTCAG		3300
GGGCAGGATC CAGGCCCTGC CAGGAAAAAT ATAAGGGCCC		3350
CAGAGGGGT CATCCACTGC ATGAGAGTGG GGATGTCACA		3400
CACCCTCCTG GTAGCACTGA GAAGCCAGGG CTGTGCTTGC		3450
CTGAGGGCCC GTGGATTCCT CTTCCTGGAG CTCCAGGAAC		3500
GGCCTTGGTC TGAGACAGTA TCCTCAGGTC ACAGAGCAGA	GGATGCACAG	3550
GGTGTGCCAG CAGTGAATGT TTGCCCTGAA TGCACACCAA	GGGCCCACC	3600
TGCCACAGGA CACATAGGAC TCCACAGAGT CTGGCCTCAC	CTCCCTACTG	3650
TCAGTCCTGT AGAATCGACC TCTGCTGGCC GGCTGTACCC	TGAGTACCCT	3700
CTCACTTCCT CCTTCAGGTT TTCAGGGGAC AGGCCAACCC	AGAGGACAGG	3750
ATTCCCTGGA GGCCACAGAG GAGCACCAAG GAGAAGATCT		3800
CTTTGTTAGA GTCTCCAAGG TTCAGTTCTC AGCTGAGGCC		3850
TCCCTCTCT CCCAGGCCTG TGGGTCTTCA TTGCCCAGCT	CCTGCCCACA	3900
CTCCTGCCTG CTGCCCTGAC GAGAGTCATC		3930
ATG TCT CTT GAG CAG AGG AGT CTG CAC TGC AAG	CCT GAG GAA	3972
GCC CTT GAG GCC CAA CAA GAG GCC CTG GGC CTG	GTG TGT GTG	4014
CAG GCT GCC ACC TCC TCC TCT CCT CTG GTC	CTG GGC ACC	4056
CTG GAG GAG GTG CCC ACT GCT GGG TCA ACA GAT	CCT CCC CAG	4098
AGT CCT CAG GGA GCC TCC GCC TTT CCC ACT ACC	ATC AAC TTC	4140
ACT CGA CAG AGG CAA CCC AGT GAG GGT TCC AGC	AGC CGT GAA	4182
GAG GAG GGG CCA AGC ACC TCT TGT ATC CTG GAG	TCC TTG TTC	4224
CGA GCA GTA ATC ACT AAG AAG GTG GCT GAT TTG	GTT GGT TTT	4266
CTG CTC CTC AAA TAT CGA GCC AGG GAG CCA GTC	ACA AAG GCA	4308
GAA ATG CTG GAG AGT GTC ATC AAA AAT TAC AAG	CAC TGT TTT	4350
CCT GAG ATC TTC GGC AAA GCC TCT GAG TCC TTG	CAG CTG GTC	4392
TTT GGC ATT GAC GTG AAG GAA GCA GAC CCC ACC		4434
TAT GTC CTT GTC ACC TGC CTA GGT CTC TCC TAT		4476
CTG GGT GAT AAT CAG ATC ATG CCC AAG ACA GGC	TTC CTG ATA	4518
ATT GTC CTG GTC ATG ATT GCA ATG GAG GGC GGC	CAT GCT CCT	4560
GAG GAG GAA ATC TGG GAG GAG CTG AGT GTG ATG	GAG GTG TAT	4602
GAT GGG AGG GAG CAC AGT GCC TAT GGG GAG CCC	AGG AAG CTG	4644
		

CTC ACC CAA GAT TTG GT	G CAG GAA AAG TAC CT	G GAG TAC GGC	4686
AGG TGC CGG ACA GTG AT	C CCG CAC GCT ATG AG	T TCC TGT GGG	4728
GTC CAA GGG CCC TCG CT	G AAA CCA GCT ATG TG	A	4761
AAGTCCTTGA GTATGTGATC	AAGGTCAGTG CAAGAGTTC	 	4800
GCTTTTTCTT CCCATCCCTG	CGTGAAGCAG CTTTGAGAG	A GGAGGAAGAG	4850
GGAGTCTGAG CATGAGTTGC	AGCCAAGGCC AGTGGGAGG	G GGACTGGGCC	4900
AGTGCACCTT CCAGGGCCGC	GTCCAGCAGC TTCCCCTGC	C TCGTGTGACA	4950
TGAGGCCCAT TCTTCACTCT	GAAGAGAGCG GTCAGTGTT	C TCAGTAGTAG	5000
GTTTCTGTTC TATTGGGTGA	CTTGGAGATT TATCTTTGT	T CTCTTTTGGA	5050
ATTGTTCAAA TGTTTTTTT	TAAGGGATGG TTGAATGAA	C TTCAGCATCC	5100
AAGTTTATGA ATGACAGCAG	TCACACAGTT CTGTGTATA	T AGTTTAAGGG	5150
TAAGAGTCTT GTGTTTTATT	CAGATTGGGA AATCCATTC	T ATTTTGTGAA	5200
TTGGGATAAT AACAGCAGTG	GAATAAGTAC TTAGAAATG	T GAAAAATGAG	5250
CAGTAAAATA GATGAGATAA	AGAACTAAAG AAATTAAGA	G ATAGTCAATT	5300
CTTGCCTTAT ACCTCAGTCT	ATTCTGTAAA ATTTTTAAA	G ATATATGCAT	5350
ACCTGGATTT CCTTGGCTTC	TTTGAGAATG TAAGAGAAA	T TAAATCTGAA	5400
TAAAGAATTC TTCCTGTTCA	CTGGCTCTTT TCTTCTCA	T GCACTGAGCA	5450
TCTGCTTTTT GGAAGGCCCT	GGGTTAGTAG TGGAGATGC	T AAGGTAAGCC	5500
AGACTCATAC CCACCCATAG	GGTCGTAGAG TCTAGGAGC	T GCAGTCACGT	5550
AATCGAGGTG GCAAGATGTC	CTCTAAAGAT GTAGGGAAA	A GTGAGAGAGG	5600
GGTGAGGGTG TGGGGCTCCG	GGTGAGAGTG GTGGAGTGT	C AATGCCCTGA	5650
GCTGGGGCAT TTTGGGCTTT	GGGAAACTGC AGTTCCTTC	T GGGGGAGCTG	5700
ATTGTAATGA TCTTGGGTGG	ATCC		5724

(2) INFORMATION FOR SEQUENCE ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4157 base pairs

(B) TYPE: nucleic acid (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

	TCCCCATCCG				50
	TCACGGGCCC				100
	CAGCGAGATT				150
	GGCGCAGGCT				200
	CGGGCCTCAC				250
	CTGCCGGGCC				300
	CACCACCTCA				350
	CGTAAGAGCT				400
	CCAGACTCAG				450
	AACCCACCCC				500
	CCCCCATCCC				550
	TCCCCCACCA				600
	ACGGAAGCTC				650
	GTACGGCTAA				700
	ATGCAGAGGA				750
	ACCCAGCATG				800
	CCACCTTTTC				850
	GGGGTTGGGG				900
	ACTGAGGGGA				950
	CCTGGGCACA				1000
	ACAGAGAGTT				1050
	GGGAGGAATC				1100
CTTCATGAGG	ACTCCCCATA	CCCCGGCCC	AGAAAGAAGG	GATGCCACAG	1150
	TAAATTGTTC				1200
	CAATCTCATT				1250
	AGGTGTTGGT				1300
GGTTCCCCCT	TGAGAAAGGG	CAGTCCCTGG	CAGGAGTAAA	GATGAGTAAC	1350
	CCATCATAAC				1400
GGACAACGCA	CGTGGGGTAA	CAGGATGTGG	CCCCTCCTCA	CTTGTCTTTC	1450
	GGAGTTGATG				1500
	CTCTGGTCGA				1550
	AGAGCCTGAG				1600
	GGCCCCATAG				1650
	CAGGGCTGTC				1700
	GAAGGGGAGG				1750
	GGTCTCAGGC				1800
	CCAGGACACC				1850
	GAGGACCTGG				1900
TCTCCTTCTG	TACCATATCA	GGGATGTGAG	TTCTTGACAT	GAGAGATTCT	1950
CAAGCCAGCA	AAAGGGTGGG	ATTAGGCCCT	ACAAGGAGAA	AGGTGAGGGC	2000
CCTGAGTGAG	CACAGAGGGG	ACCCTCCACC	CAAGTAGAGT	GGGGACCTCA	2050

CGGAGTCTGG CCAACCCTGC TGAGACTTCT GGGAATCCGT		2100
GCAGTCTGCA CACTGAAGGC CCGTGCATTC CTCTCCCAGG	AATCAGGAGC	2150
TCCAGGAACC AGGCAGTGAG GCCTTGGTCT GAGTCAGTGC	CTCAGGTCAC	2200
AGAGCAGAGG GGACGCAGAC AGTGCCAACA CTGAAGGTTT		2250
CACACCAAGG GCCCCACCG CCCAGAACAA ATGGGACTCC		2300
GCCTCACCCT CCCTATTCTC AGTCCTGCAG CCTGAGCATG		2350
CTGTACCCTG AGGTGCCCTC CCACTTCCTC CTTCAGGTTC		2400
AGGCTGACAA GTAGGACCCG AGGCACTGGA GGAGCATTGA		2450
CTGTAAGTAA GCCTTTGTCA GAGCCTCCAA GGTTCAGTTC	AGTTCTCACC	2500
TAAGGCCTCA CACACGCTCC TTCTCTCCCC AGGCCTGTGG	GTCTTCATTG	2550
CCCAGCTCCT GCCCGCACTC CTGCCTGCTG CCCTGACCAG	AGTCATC	2597
ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG	CCT GAA GAA	2639
GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG		
		2681
CAG GCT CCT GCT ACT GAG GAG CAG ACC GCT		2723
TCT ACT CTA GTG GAA GTT ACC CTG GGG GAG GTG		2765
GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA		2807
TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA	CAA TCC GAT	2849
GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA	AGA ATG TTT	2891
CCC GAC CTG GAG TCC GAG TTC CAA GCA GCA ATC		2933
ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG		2975
AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG		
		3017
AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC		3059
TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG		3101
GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC		3143
GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT	CAG GTC ATG	3185
CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GCC	ATA ATC GCA	3227
ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC		3269
CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAG		3311
TTC GCA CAT CCC AGG AAG CTG CTC ATG CAA GAT		
GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC		3353
CON TICO THE CAG HAT OFFE THE CAG CAG GTG CCC GGC	AGT GAT CCT	3395
GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC	CTC ATT GAA	3437
ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT	AAG ATC GGT	3479
GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT	GAA CGG GCT	3521
- 11"1" AGA GAG GGA GXX GXC MGX		3542
GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT	CTGGGCCAGT	3592
GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG	ТСТСАТАТСА	3642
GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT	TACCACTCAC	3692
TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT	CCTCTTCCAA	
TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT		3742
		3792
GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT		3842
TAAGAGTCCT GTTTTTTATT CAGATTGGGA AATCCATTCC		3892
TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT		3942
AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT	AGTTAATTCT	3992
TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG		4042
TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA		4092
TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC		
CCTGGTAGTA GTGGG	IGIGGMAGGC	4142
CCIGGINGIA GIGGG		4157

- (2) INFORMATION FOR SEQUENCE ID NO: 10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 662 base pairs
 - (B) TYPE: nucleic acid (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-21 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGATCCCCAT	GGATCCAGGA	AGAATCCAGT	TCCACCCCTG	CTGTGAACCC	50
AGGGAAGTCA	CGGGGCCGGA	TGTGACGCCA	CTGACTTGCG	CGTTGGAGGT	100
CAGAGAACAG	CGAGATTCTC	GCCCTGAGCA	ACGGCCTGAC	GTCGGCGGAG	150
GGAAGCAGGC	GCAGGCTCCG	TGAGGAGGCA	AGGTAAGATG	CCGAGGGAGG	200
ACTGAGGCGG	GCCTCACCCC	AGACAGAGGG	CCCCCAATAA	TCCAGCGCTG	250
CCTCTGCTGC	CAGGCCTGGA	CCACCCTGCA	GGGGAAGACT	TCTCAGGCTC	300
AGTCGCCACC	ACCTCACCCC	GCCACCCCC	GCCGCTTTAA	CCGCAGGGAA	350
CTCTGGTGTA	AGAGCTTTGT	GTGACCAGGG	CAGGGCTGGT	TAGAAGTGCT	400
CAGGGCCCAG	ACTCAGCCAG	GAATCAAGGT	CAGGACCCCA	AGAGGGGACT	450
GAGGGTAACC	CCCCCCCACC	CCCACCACCA	TTCCCATCCC	CCAACACCAA	500
CCCCACCCC	ATCCCCCAAC	ACCAAACCCA	CCACCATCGC	TCAAACATCA	550
ACGGCACCCC	CAAACCCCGA	TTCCCATCCC	CACCCATCCT	GGCAGAATCG	600
GAGCTTTGCC	CCTGCAATCA	ACCCACGGAA	GCTCCGGGAA	TGGCGGCCAA	650
GCACGCGGAT	CC				662

- (2) INFORMATION FOR SEQUENCE ID NO: 11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1640 base pairs
 - (B) TYPE: nucleic acid (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (ix) FEATURE:
 - (A) NAME/KEY: cDNA MAGE-3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

	50
GCCGCGAGGG AAGCCGGCCC AGGCTCGGTG AGGAGGCAAG GTTCTGAGGG GACAGGCTGA CCTGGAGGAC CAGAGGCCCC CGGAGGAGCA CTGAAGGAGA	100
	150
	171
	213
	255
	297
	339
414 mat 441 atm 447 atm 447 atm 447 atm 447	381
CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT	423
GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC	465
CCT GAC CTG GAG TCC GAG TTC CAA GCA GCA CTC AGT AGG AAG	507
GTG GCC GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC	549
AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC	591
GGA AAT TGG CAG TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT	633
TCC AGT TCC TTG CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA	675
	717
GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG	759
	801
AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG	843
CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG	885
TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG	927
GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT	969
GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA	011
ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT	053
GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT	095
TTG AGA GAG GGG GAA GAG TGA	116
GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT 1	166
GCACCTTCCG GGGCCGCATC CCTTAGTTTC CACTGCCTCC TGTGACGTGA 1:	216
GGCCCATTCT TCACTCTTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG	266
TTTCTGTTCT GTTGGATGAC TTTGAGATTA TTCTTTGTTT CCTGTTGGAG 1:	316
TTGTTCAAAT GTTCCTTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG	366
GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGAG	416
	466
TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC	516
GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG	566
	616
ACCAGGATTT CCTTGACTTC TTTG	640

- (2) INFORMATION FOR SEQUENCE ID NO: 12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 943 base pairs
 - (B) TYPE: nucleic acid (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-31 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGATCCTCCA	CCCC	AGTAG	A GI	rggg	SACCI	CAC	CAGAC	TCT	GGC	CAAC	CCT	50
CCTGACAGTT	CTGG	GAATC	C GI	rggci	rgcgi	TTC	CTG	CTG	CAC	ATTGO	GGG	100
GCCCGTGGAT												150
AGGACTTGGT	CTGA	GGCAG	T GT	CCTC	CAGGI	CAC	CAGAC	TAG	AGG	GgC	ГCA	200
GATAGTGCCA	ACGG	rgaa g	G TI	TGC	CTTGG	TA :	CAA	ACCA	AGG	GCCC	CAC	250
CTGCCCCAGA	ACAC	ATGGA	C TO	CAG	AGCGC	CTC	GCCI	CAC	CCT	CAATA	ACT	300
TTCAGTCCTG	CAGC	CTCAG	C AT	rgcgc	CTGGC	CGG	SATG	CACC	CTG	AGGT	GCC	350
CTCTCACTTC	CTCC	TTCAG	G TI	CTG <i>I</i>	AGGGG	ACA	AGGCT	CGAC	CTG	SAGG	ACC	400
AGAGGCCCCC	GGAG	GAGCA	C TC	AAGO	GAGAA	GAT	CTG	PAAG	TAAC	CCT	ГTG	450
TTAGAGCCTC	CAAG	GTTCC	A TI	CAG	PACTO	AGO	CTGAC	GTC	TCT	CACA	rgc	500
TCCCTCTCTC	CCCA	GGCCA	G TO	GGT	CTCCA	TTC	CCCI	AGCT	CCTC	GCCC	ACA	550
CTCCCGCCTG	TTGC	CCTGA	C CA	GAG	CATC	2						580
ATG CCT CT												622
GGC CTT GA												664
CAG GCT CC												706
TCT AGT GT												748
GAG TCA CC												790
CTC CCC AC												832
GAG GAC TC												874
CCT GAC CT							GCA	CTC	AGT	AGG	AAG	916
GTG GCC AA	G TTG	GTT	CAT	TTT	CTG	CTC						943

- (2) INFORMATION FOR SEQUENCE ID NO: 13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1067 base pairs
 - (B) TYPE: nucleic acid (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (ix) FEATURE:
 - (A) NAME/KEY: cDNA MAGE-4
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

	GGG		AGC										CGA	39
GAA	GCA	CTC	AGT	AAC	AAG	GTG	GAT	GAG	TTG	GCT	CAT	TTT	CTG	81
CTC	CGC	AAG	TAT	CGA	GCC	AAG	GAG	CTG	GTC	ACA	AAG	GCA	GAA	123
ATG	CTG	GAG	AGA	GTC	ATC	AAA	AAT	TAC	AAG	CGC	TGC	TTT	CCT	165
GTG	ATC	TTC	GGC	AAA	GCC	TCC	GAG	TCC	CTG	AAG	ATG	ATC	TTT	207
GGC	ATT	GAC	GTG	AAG	GAA	GTG	GAC	CCC	GCC	AGC	AAC	ACC	TAC	249
ACC	CTT	GTC	ACC	TGC	CTG	GGC	CTT	TCC	TAT	GAT	GGC	CTG	CTG	291
GGT	AAT	AAT	CAG	ATC	TTT	CCC	AAG	ACA	GGC	CTT	CTG	ATA	ATC	333
GTC	CTG	GGC	ACA	ATT	GCA	ATG	GAG	GGC	GAC	AGC	GCC	TCT	GAG	375
GAG	GAA	ATC	TGG	GAG	GAG	CTG	GGT	GTG	ATG	GGG	GTG	TAT	GAT	417
			CAC											459
			TGG											501
GTA	CCC	GGC	AGT	AAT	CCT	GCG	CGC	TAT	GAG	TTC	CTG	TGG	GGT	543
CCA	AGG	GCT	CTG	GCT	GAA	ACC	AGC	TAT	GTG	AAA	GTC	CTG	GAG	585
	GTG		AGG											627
			GAA											669
			rtgc <i>i</i>											719
			AGCC											769
			CACTO											819
			rgttc											869
			rgtt											919
AGT	TAT		rcgt <i>i</i>											969
	\GTC1		PTTTI											1019
TTG	GAC	ATA A	ATAAC	CAGC	AG TO	GAG	raagi	r ATI	TAG!	AAGT	GTG	ATTO	2	1067

(2)	INFORMATION FOR SEQUENCE ID NO: 14:
•	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 226 base pairs
	(B) TYPE: nucleic acid
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: genomic DNA
	(ix) FEATURE:
	(A) NAME/KEY: MAGE-5 gene
	(xi) SEQUENCE DESCRIPTION: SEO ID NO: 14:

,

AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG	
AAGCCTTTGT TAGAGCCTCC AAGGTTCAGT TTTTAGCTGA	GGCTTCTCAC 100
ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC	AGCTCCTGCC 150
CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC	184
ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG	CCT GAG GAA 226

1

(2)	INFORMATION FOR SEQUENCE ID NO: 15:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 225 base pairs
	(B) TYPE: nucleic acid
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: cDNA
	(ix) FEATURE:
	(A) NAME/KEY: MAGE-6 gene
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TAT	TTC	TTT	CCT	GTG	ATC	TTC	AGC	AAA	GCT	TCC	GAT	TCC	TTG	42
CAG	CTG	GTC	TTT	GGC	ATC	GAG	CTG	ATG	GAA	GTG	GAC	CCC	ATC	84
GGC	CAC	GTG	TAC	ATC	TTT	GCC	ACC	TGC	CTG	GGC	CTC	TCC	TAC	126
GAT	GGC	CTG	CTG	GGT	GAC	AAT	CAG	ATC	ATG	CCC	AGG	ACA	GGC	168
TTC	CTG	ATA	ATC	ATC	CTG	GCC	ATA	ATC	GCA	AGA	GAG	GGC	GAC	210
TGT	GCC	CCT	GAG	GAG										225

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(2) INFORMATION FOR SEQUENCE ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 base pairs
 - (B) TYPE: nucleic acid (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: MAGE-7 gene
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ACA	AGC	ACT	AGT'	TTC	CTT	GTG	ATC	TAT	GGC	AAA	GCC	TCA	GAG	42
TGC	ATG	CAG	GTG	ATG	TTT	GGC	ATT	GAC	ATG	AAG	GAA	GTG	GAC	84
CCC	GCG	GCC	ACT	CCT	ACG	TCT	TGT	ACC	TGC	TTG	GGC	CTC	TCC	126
TAC	AAT	GGC	CTG	CTG	GGT	GAT	GAT	CAG	AGC	ATG	CCC	GAG	A	166

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Boon, Thierry, Van den Eynde, Benoît
- (ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor Rejection Antigens and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Felfe & Lynch
 - (B) STREET: 805 Third Avenue
 - (C) CITY: New York City
 - (D) STATE: New York
 - (F) ZIP: 10022
- (V) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 - (B) COMPUTER: IBM
 - (C) OPERATING SYSTEM: PC-DOS
 - (D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/807,043
 - (B) FILING DATE: 12-DECEMBER-1991
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/764,364
 - (B) FILING DATE: 23-SEPTEMBER-1991
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/728,838
 - (B) FILING DATE: 9-JULY-1991
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/705,702
 - (B) FILING DATE: 23-May-1991
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hanson, Norman D.
 - (B) REGISTRATION NUMBER: 30,946
 - (C) REFERENCE/DOCKET NUMBER: LUD 253.3
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 688-9200
 - (B) TELEFAX: (212) 838-3884

- (2) INFORMATION FOR SEQUENCE ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 (C) STRANDEDNESS: singular
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACCACAGGAG	AATGAAAAGA	ACCCGGGACT	CCCAAAGACG	CTAGATGTGT	GAAGATCCTG	60
ATCACTCATT	GGGTGTCTGA	GTTCTGCGAT	ATTCATCCCT	CAGCCAATGA	GCTTACTGTT	120
CTCGTGGGGG	GTTTGTGAGC	CTTGGGTAGG	AAGTTTTGCA	AGTTCCGCCT	ACAGCTCTAG	180
CTTGTGAATT	TGTACCCTTT	CACGTAAAAA	AGTAGTCCAG	AGTTTACTAC	ACCCTCCCTC	240
CCCCCTCCCA	CCTCGTGCTG	TGCTGAGTTT	AGAAGTCTTC	CTTATAGAAG	TCTTCCGTAT	300
AGAACTCTTC	CGGAGGAAGG	AGGGAGGACC	CCCCCCTTT	GCTCTCCCAG	CATGCATTGT	360
GTCAACGCCA	TTGCACTGAG	CTGGTCGAAG	AAGTAAGCCG	CTAGCTTGCG	ACTCTACTCT	420
TATCTTAACT	TAGCTCGGCT	TCCTGCTGGT	ACCCTTTGTG	CC		462

(i)	() () ()	A) LI B) TY C) ST O) TO	PE: PANI POLO	nuc DEDNI DGY:	lir	c aci sin near	id igula	ar					
(xi	i) SI	EQUE	ICE I	DESCI	RIPT	ON:	SEÇ) ID	NO:	2:			
TCT Ser													48
GGT Gly													96
ATT Ile													144
TTT Phe 50													192
GAA Glu													240
GTC Val													288
GAC Asp													336
GAA Glu													384
GAA Glu 130													432
GCT Ala													480
GAA Glu													528

INFORMATION FOR SEQUENCE ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(2)

	 	 	 AAC Asn	 	 	 	 	 576
	 	 	 GTT Val	 	 	 	 	 624
	 	 	 GAA Glu	 	 	 	 	 672
TAG								675

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(2)	INF	ORMATION	FOR	SEQUENCE	ID NO:	3 :
	(i)	SEQUENCE	E CHA	RACTERIST	rics:	

- (A) LENGTH: 228 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear (ii) MOLECULE TYPE: genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCATGCAGTT	GCAAAGCCCA	GAAGAAAGAA	ATGGACAGCG	GAAGAAGTGG	TTGTTTTTTT	60
TTCCCCTTCA	TTAATTTTCT	AGTTTTTAGT	AATCCAGAAA	ATTTGATTTT	GTTCTAAAGT	120
TCATTATGCA	AAGATGTCAC	CAACAGACTT	CTGACTGCAT	GGTGAACTTT	CATATGATAC	180
ATAGGATTAC	ACTTGTACCT	GTTAAAAATA	AAAGTTTGAC	TTGCATAC		228

- (2) INFORMATION FOR SEQUENCE ID NO: 4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1365 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear (ii) MOLECULE TYPE: genomic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT	50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT	100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG	150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT	200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA	250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT	300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG	350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG	400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT	450
ACCCTTTGTG CC	462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA	504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG	546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
GAT GAA GAC GAT GAG GAT GAG GAT GAC TAC TAC GAC GAC	756
GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	798
GAG GAA GAA TTG GAG AAC CTG ATG GAT GAA TCA GAA	840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT	924
GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG AT	966
TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG	1008
AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT	1050
GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG	1092
GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT	1134
TAG	1137
GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG	1187
TTGTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA	1237
ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT	1287
CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT	1337
GTTAAAAATA AAAGTTTGAC TTGCATAC	1365

- (2) INFORMATION FOR SEQUENCE ID NO: 5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4698 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCC	CAAAGACG CTAGATGTGT 50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GT	
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GT	
	IGTGAATT TGTACCCTTT 200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACC	
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CT	
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCG	
CATGCATTGT GTCAACGCCA TTGCACTGAG CTC	
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAG	
ACCCTTGGG ACTCTACTCT TATCTTAACT TAC	
	462
ATG TCT GAT AAC AAG AAA CCA GAC AAA	
GGT GGT GAC GGT GAT GGG AAT AGG TGC	
TAC TCC CTG GAA GAA ATT CTG CCT TAT	
TTC GCT GTT GTC ACA ACA AGT TTT CTG	
TGG ATA GCC AGG CAA AGC AAG CGC ATG	
GAG GAC GAC GAC GAT GCC TTC TAT	
GAG GAA GAA TTG GAG AAC CTG ATG	
GAT GAG GCC GAA GAA GAG ATG AGC GTG	
GCT GAG GAA ATG GGT GCT GGC GCT AAC	
GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAG	GGTGGGGT GCATTCTTTA 966
CTCTTGCCCA CATCTGTAGT AAAGACCACA TT	TTGGTTGG GGGTCATTGC 1016
TGGAGCCATT CCTGGCTCTC CTGTCCACGC CT	ATCCCCGC TCCTCCCATC 1066
CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCC	CCACCTTG CCTCTGGAGC 1116
TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CT	TTGCTCTC CTTGCTCCCC 1166
TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCT	TCTCTGAT CCCCACCCTC 1216
TTCAGGCTTC CCCATTTGCT CCTCTCCCGA AAG	CCCTCCCC TTCCTGTTCC 1266
CCTTTTCGCG CCTTTTCTTT CCTGCTCCCC TC	CCCCTCCC TATTTACCTT 1316
TCACCAGCTT TGCTCTCCCT GCTCCCCTCC CC	CTTTTGCA CCTTTTCTTT 1366
TCCTGCTCCC CTCCCCTCT TAG	CCCTTCAC CGCTTTTCCT 1416
CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCC	CCTATTTG CATTTTCGGG 1466
	TTTGCATT TTCGGGTGCT 1516
CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TT	TTTTTTT TTTTTTTTT 1566
TTGGTTTTTC GAGACAGGGT TTCTCTTTGT ATO	
TCACTCTGTA GACCAGGCTG GCCTCAAACT CAG	
CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CC	
GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAX	
	CCCCCTCC CCCTCCTGT 1816
	GTTCCCTC TCCCTGCTCC 1866
CCTCCCCTC TTTGCTCGAC TTTTAGCAGC CT	
GCCCGTTCC CCTTTTTTGT GCCTTTCCTC CTC	
	1700

AGCTCACCTT TTTGTTTGTT TGGTTGTTTG GTTGTTTGGT	TTGCTTTTTT	2016
TTTTTTTTT GCACCTTGTT TTCCAAGATC CCCCTCCCCC	TCCGGCTTCC	2066
CCTCTGTGTG CCTTTCCTGT TCCCTCCCCC TCGCTGGCTC	CCCCTCCCTT	2116
TCTGCCTTC CTGTCCCTGC TCCCTTCTCT GCTAACCTTT	TAATGCCTTT	2166
CTTTTCTAGA CTCCCCCCTC CAGGCTTGCT GTTTGCTTCT	GTGCACTTTT	2216
CCTGACCCTG CTCCCCTTCC CCTCCCAGCT CCCCCCTCTT	TTCCCACCTC	2266
CCTTTCTCCA GCCTGTCACC CCTCCTTCTC TCCTCTCTGT	TTCTCCCACT	2316
TCCTGCTTCC TTTACCCCTT CCCTCTCCT ACTCTCCTCC	CTGCCTGCTG	2366
GACTTCCTCT CCAGCCGCCC AGTTCCCTGC AGTCCTGGAG	TCTTTCCTGC	2416
CTCTCTGTCC ATCACTTCCC CCTAGTTTCA CTTCCCTTTC	ACTCTCCCCT	2466
ATGTGTCTCT CTTCCTATCT ATCCCTTCCT TTCTGTCCCC	TCTCCTCTGT	2516
CCATCACCTC TCTCCTCCT TCCCTTTCCT CTCTCTTCCA		2566
CCTGCTTCTT TACCCTGCCT CTCCCATTGC CCTCTTACCT		2616
TCCATGTCCC CTCTCAATTC CCTGTCCCAT TGTGCTCCCT		2666
ATTTCCCTCT TTCTCCCTTA GCCTCTTCTT CCTCTTCTCT		2716
TTCCCTTTGC TTCTCCCTCC TCCTTTCCCC TTCCCCTATG		2766
TACTTGATCT TCTCTCCTCT CCACATACCC TTTTTCCTTT		2816
CTTTGTCCCC AGACCCTACA GTATCCTGTG CACAGGAAGT		2866
ATCAACAACA AGGAGGCAAG AAACAGAGCA AAATCCCAAA	ATCAGCAGGA	2916
AAGGCTGGAT GAAAATAAGG CCAGGTTCTG AGGACAGCTG	GAATCTAGCC	2966
AAGTGGCTCC TATAACCCTA AGTACCAAGG GAGAAAGTGA	TGGTGAAGTT	3016
CTTGATCCTT GCTGCTTCTT TTACATATGT TGGCACATCT	TTCTCAAATG	3066
CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA	AGTAATGGGA	3116
GAATCTGAAA ACTAGGGGCC AGTGGTTTGT TTTGGGGACA	AATTAGCACG	3166
TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA	TGATTTGAGA	3216
TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA	GTTCTTTTTA	3266
	CTGCTTTCTT	3316
TTGCTAAAAT ATTCTTTCTC ACATATTCAT ATTCTCCAG		3355
GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA	GTG AAG TGT	3396
	CTG GTG TCT	3438
ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT		3480
AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA		3522
GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC		3564
TTC TCA CCT TAG	CCG GAI GGC	3576
GCATGCAGGT ACTGGCTTCA CTAACCAACC ATTCCTAACA	MA MCCCMCMA	3626
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA		
TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA		3676
		3726
CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT		3776
GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT		3826
GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA		3876
TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA		3926
TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT		3976
TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG		4026
CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT		4076
TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTTA		4126
AATGTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA		4176
GTAACTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA	GCAATAGGGA	4226
GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC	AGGCCCTTGC	4276
CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC	TCTCCAAATC	4326
ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA	ACAGGGAAAT	4376
ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA		4426
AGTCAGGAGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT		4476
AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA		4526
TTTTTTCCCC TTCATTAATT TTCTAGTTTT TAGTAATCCA	GAAAATTTGA	4576

TTTTGTTCTA	AAGTTCATTA	TGCAAAGATG	TCACCAACAG	ACTTCTGACT	4626
GCATGGTGAA	CTTTCATATG	ATACATAGGA	TTACACTTGT	ACCTGTTAAA	4676
AATAAAAGTT	TGACTTGCAT	AC			4698

- (2) INFORMATION FOR SEQUENCE ID NO: 6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids

 - (B) TYPE: amino acid (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu

- (2) INFORMATION FOR SEQUENCE ID NO: 7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2419 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear (ii) MOLECULE TYPE: genomic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCAGGC	CCTGCCAGGA	AAAATATAAG	GGCCCTGCGT	GAGAACAGAG	50
GGGGTCATCC	ACTGCATGAG	AGTGGGGATG	TCACAGAGTC	CAGCCCACCC	100
TCCTGGTAGC	ACTGAGAAGC	CAGGGCTGTG	CTTGCGGTCT	GCACCCTGAG	150
GGCCCGTGGA	TTCCTCTTCC	TGGAGCTCCA	GGAACCAGGC	AGTGAGGCCT	200
TGGTCTGAGA	CAGTATCCTC	AGGTCACAGA	GCAGAGGATG	CACAGGGTGT	250
GCCAGCAGTG	AATGTTTGCC	CTGAATGCAC	ACCAAGGGCC	CCACCTGCCA	300
CAGGACACAT	AGGACTCCAC	AGAGTCTGGC	CTCACCTCCC	TACTGTCAGT	350
CCTGTAGAAT	CGACCTCTGC	TGGCCGGCTG	TACCCTGAGT	ACCCTCTCAC	400
TTCCTCCTTC	AGGTTTTCAG	GGGACAGGCC	AACCCAGAGG	ACAGGATTCC	450
CTGGAGGCCA	CAGAGGAGCA	CCAAGGAGAA	GATCTGTAAG	TAGGCCTTTG	500
TTAGAGTCTC	CAAGGTTCAG	TTCTCAGCTG	AGGCCTCTCA	CACACTCCCT	550
CTCTCCCCAG	GCCTGTGGGT	CTTCATTGCC	CAGCTCCTGC	CCACACTCCT	600
GCCTGCTGCC		TCATCATGTC		AGGAGTCTGC	650
ACTGCAAGCC	TGAGGAAGCC	CTTGAGGCCC	AACAAGAGGC	CCTGGGCCTG	700
GTGTGTGTGC		CTCCTCCTCC	TCTCCTCTGG	TCCTGGGCAC	750
CCTGGAGGAG	GTGCCCACTG	CTGGGTCAAC	AGATCCTCCC	CAGAGTCCTC	800
AGGGAGCCTC	CGCCTTTCCC	ACTACCATCA	ACTTCACTCG	ACAGAGGCAA	850
CCCAGTGAGG	GTTCCAGCAG	CCGTGAAGAG	GAGGGGCCAA	GCACCTCTTG	900
TATCCTGGAG	TCCTTGTTCC	GAGCAGTAAT	CACTAAGAAG	GTGGCTGATT	950
TGGTTGGTTT	TCTGCTCCTC	AAATATCGAG	CCAGGGAGCC	AGTCACAAAG	1000
GCAGAAATGC	TGGAGAGTGT	CATCAAAAAT	TACAAGCACT	GTTTTCCTGA	1050
		AGTCCTTGCA		GGCATTGACG	1100
TGAAGGAAGC	AGACCCCACC	GGCCACTCCT	ATGTCCTTGT	CACCTGCCTA	1150
-	ATGATGGCCT	GCTGGGTGAT	AATCAGATCA	TGCCCAAGAC	1200
AGGCTTCCTG	ATAATTGTCC	TGGTCATGAT	TGCAATGGAG	GGCGGCCATG	1250
CTCCTGAGGA	GGAAATCTGG	GAGGAGCTGA	GTGTGATGGA	GGTGTATGAT	1300
GGGAGGGAGC	ACAGTGCCTA	TGGGGAGCCC	AGGAAGCTGC	TCACCCAAGA	1350
TTTGGTGCAG	GAAAAGTACC	TGGAGTACGG	CAGGTGCCGG	ACAGTGATCC	1400
CGCACGCTAT	GAGTTCCTGT	GGGGTCCAAG	GGCCCTCGCT	GAAACCAGCT	1450
ATGTGAAAGT	CCTTGAGTAT	GTGATCAAGG	TCAGTGCAAG	AGTTCGCTTT	1500
TTCTTCCCAT		AGCAGCTTTG		AAGAGGGAGT	1550
CTGAGCATGA		AGGCCAGTGG		GGGCCAGTGC	1600
ACCTTCCAGG		GCAGCTTCCC	CTGCCTCGTG	TGACATGAGG	1650
CCCATTCTTC	ACTCTGAAGA	GAGCGGTCAG	TGTTCTCAGT	AGTAGGTTTC	1700
TGTTCTATTG		AGATTTATCT		TTGGAATTGT	1750
TCAAATGTTT		GATGGTTGAA		CATCCAAGTT	1800
	AGCAGTCACA		TATATAGTTT	AAGGGTAAGA	1850
GTCTTGTGTT		TGGGAAATCC		GTGAATTGGG	1900
ATAATAACAG		AGTACTTAGA	AATGTGAAAA	ATGAGCAGTA	1950
AAATAGATGA		TAAAGAAATT	AAGAGATAGT	CAATTCTTGC	2000
CTTATACCTC	AGTCTATTCT	GTAAAATTTT	TAAAGATATA	TGCATACCTG	2050

GATTTCCTTG	GCTTCTTTGA	GAATGTAAGA	GAAATTAAAT	CTGAATAAAG	2100
AATTCTTCCT	GTTCACTGGC	TCTTTTCTTC	TCCATGCACT	GAGCATCTGC	2150
TTTTTGGAAG	GCCCTGGGTT	AGTAGTGGAG	ATGCTAAGGT	AAGCCAGACT	2200
CATACCCACC	CATAGGGTCG	TAGAGTCTAG	GAGCTGCAGT	CACGTAATCG	2250
AGGTGGCAAG	ATGTCCTCTA	AAGATGTAGG	GAAAAGTGAG	AGAGGGGTGA	2300
GGGTGTGGGG	CTCCGGGTGA	GAGTGGTGGA	GTGTCAATGC	CCTGAGCTGG	2350
GGCATTTTGG	GCTTTGGGAA	ACTGCAGTTC	CTTCTGGGGG	AGCTGATTGT	2400
AATGATCTTG	GGTGGATCC				2419

(2) INFORMATION FOR SEQUENCE ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5674 base pairs

(B) TYPE: nucleic acid (C) STRANDEDNESS: singular

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-1 gene (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CCCGGGGCAC	CACTGGCATC	CCTCCCCTA	CCACCCCAA	TCCCTCCCTT	50
TACGCCACCC	ATCCAAACAT	CTTCACGCTC	ACCCCCAGCC	CAAGCCAGGC	100
AGAATCCGGT	TCCACCCCTG	CTCTCAACCC	AGGGAAGCCC	AGGTGCCCAG	150
ATGTGACGCC	ACTGACTTGA	GCATTAGTGG	TTAGAGAGAA	GCGAGGTTTT	200
CGGTCTGAGG	GGCGGCTTGA	GATCGGTGGA	GGGAAGCGGG	CCCAGCTCTG	250
TAAGGAGGCA	AGGTGACATG	CTGAGGGAGG	ACTGAGGACC	CACTTACCCC	300
AGATAGAGGA	CCCCAAATAA	TCCCTTCATG	CCAGTCCTGG	ACCATCTGGT	350
GGTGGACTTC	TCAGGCTGGG	CCACCCCAG	CCCCCTTGCT	GCTTAAACCA	400
	GAAGTCAGAG				450
	GTCCAGGCTC				500
AGGGCTGAGG	GTCCCTAAGA	CCCCACTCCC	GTGACCCAAC	CCCCACTCCA	550
ATGCTCACTC	CCGTGACCCA	ACCCCCTCTT	CATTGTCATT	CCAACCCCCA	600
CCCCACATCC	CCCACCCCAT	CCCTCAACCC	TGATGCCCAT	CCGCCCAGCC	650
ATTCCACCCT	CACCCCACC	CCCACCCCA	CGCCCACTCC	CACCCCCACC	700
	CCGGTTCCCG				750
GCCACTGACT	TGCGCATTGT	GGGGCAGAGA	GAAGCGAGGT	TTCCATTCTG	800
	TAGAGTTCGG				850
	AGAGGCTGAG				900
	AATATTCCAG				950
	CGTCTCAGCC				1000
	CACCAGGTTC				1050
	GCAGGACTGG				1100
GGCATCAAGA	TCAGCACCCA	AGAGGGAGGG	CTGTGGGCCC	CCAAGACTGC	1150
ACTCCAATCC	CCACTCCCAC	CCCATTCGCA	TTCCCATTCC	CCACCCAACC	1200
	CAGCTACACC				1250
	ACCCTCCAGC				1300
TCACCCTCAC	TGCCCCCAAC	CCCACCCTCA	TCTCTCTCAT	GTGCCCCACT	1350
	CCCCCATTCT		-		1400
	CCTGGTAGGC				1450
	GAAGCCAGGT				1500
	GGGAGTGGTT				1550
	ACTGAGGAGG				1600
	ACCCCTGCTG				1650
	GACCACCCC				1700
	AGTCATAGCT				1750
	AGGCATCAAG				1800
	GGAACTGAGG				1850
	CCACTCACAT				1900
	ATCCCTGCTG				1950
CAGGCACTCG	GATCTTGACG	TCCCCATCCA	GGGTCTGATG	GAGGGAAGGG	2000

GCTTGAACAG GGCCTCAGGG GAGCAGAGGG AGGGCCCTAC	TGCGAGATGA	2050
GGGAGGCCTC AGAGGACCCA GCACCCTAGG ACACCGCACC	CCTGTCTGAG	2100
ACTGAGGCTG CCACTTCTGG CCTCAAGAAT CAGAACGATG	GGGACTCAGA	2150
TTGCATGGGG GTGGGACCCA GGCCTGCAAG GCTTACGCGG	AGGAAGAGGA	2200
GGGAGGACTC AGGGGACCTT GGAATCCAGA TCAGTGTGGA	CCTCGGCCCT	2250
GAGAGGTCCA GGGCACGGTG GCCACATATG GCCCATATTT		2300
TGAGGTGACA GGACAGAGCT GTGGTCTGAG AAGTGGGGCC		2350
AGAGGGAGGA GTTCCAGGAT CCATATGGCC CAAGATGTGC		2400
AGGACTGGGG ATATCCCCGG CTCAGAAAGA AGGGACTCCA		2450
CTGTCCCCTT TTAGTAGCTC TAGGGGGACC AGATCAGGGA		2500
TTCCATTCTC ACTTGTACCA CAGGCAGGAA GTTGGGGGGG		2550
ATGGGGTCTT GGGGTAAAGG GGGGATGTCT ACTCATGTCA		2600
GGTTGAGGAA GCACAGGCGC TGGCAGGAAT AAAGATGAGT		
		2650
AGGCTATTGG AATCCACAC CCAGAACCAA AGGGGTCAGC		2700
TCACCCAGGA TGTGGCTTCT TTTTCACTCC TGTTTCCAGA		2750
GTGAGGACCT CATTCTCAGA GGGTGACTCA GGTCAACGTA		2800
TCTGGTCTAA AGACAGAGCG GTCCCAGGAT CTGCCATGCG		2850
GAACATGAGG GAGGACTGAG GGTACCCCAG GACCAGAACA		2900
CTGCACAGAA ATCAGCCCTG CCCCTGCTGT CACCCCAGAG		2950
GGGCCGTCTG CCGAGGTCCT TCCGTTATCC TGGGATCATT		3000
ACGGGGAGGC CTTGGTCTGA GAAGGCTGCG CTCAGGTCAG		3050
GTCCCAGGCC CTGCCAGGAG TCAAGGTGAG GACCAAGCGG		3100
CAGGACACAT TAATTCCAAT GAATTTTGAT ATCTCTTGCT	GCCCTTCCCC	3150
AAGGACCTAG GCACGTGTGG CCAGATGTTT GTCCCCTCCT		3200
TCCTTATCAT GGATGTGAAC TCTTGATTTG GATTTCTCAG	ACCAGCAAAA	3250
GGGCAGGATC CAGGCCCTGC CAGGAAAAAT ATAAGGGCCC	TGCGTGAGAA	3300
CAGAGGGGT CATCCACTGC ATGAGAGTGG GGATGTCACA	GAGTCCAGCC	3350
CACCCTCCTG GTAGCACTGA GAAGCCAGGG CTGTGCTTGC	GGTCTGCACC	3400
CTGAGGGCCC GTGGATTCCT CTTCCTGGAG CTCCAGGAAC	CAGGCAGTGA	3450
GGCCTTGGTC TGAGACAGTA TCCTCAGGTC ACAGAGCAGA	GGATGCACAG	3500
GGTGTGCCAG CAGTGAATGT TTGCCCTGAA TGCACACCAA	GGGCCCACC	3550
TGCCACAGGA CACATAGGAC TCCACAGAGT CTGGCCTCAC		3600
TCAGTCCTGT AGAATCGACC TCTGCTGGCC GGCTGTACCC	TGAGTACCCT	3650
CTCACTTCCT CCTTCAGGTT TTCAGGGGAC AGGCCAACCC		3700
ATTCCCTGGA GGCCACAGAG GAGCACCAAG GAGAAGATCT		3750
CTTTGTTAGA GTCTCCAAGG TTCAGTTCTC AGCTGAGGCC		3800
TCCCTCTCTC CCCAGGCCTG TGGGTCTTCA TTGCCCAGCT		3850
CTCCTGCCTG CTGCCCTGAC GAGAGTCATC	COTOCCACA	3880
ATG TCT CTT GAG CAG AGG AGT CTG CAC TGC AAG	CCT GAG GAA	3922
GCC CTT GAG GCC CAA CAA GAG GCC CTG GGC CTG		3964
CAG GCT GCC ACC TCC TCC TCT CCT CTG GTC		4006
CTG GAG GAG GTG CCC ACT GCT GGG TCA ACA GAT		
AGT CCT CAG GGA GCC TCC GCC TTT CCC ACT ACC		4048 4090
ACT CGA CAG AGG CAA CCC AGT GAG GGT TCC AGG		
GAG GAG GGG CCA AGC ACC TCT TGT ATC CTG GAG		4132
CGA GCA GTA ATC ACT AAG AAG GTG GCT GAT TTG		4174
CTG CTC CTC AAA TAT CGA GCC AGG GAG CCA GTC		4216
		4258
GAA ATG CTG GAG AGT GTC ATC AAA AAT TAC AAG		4300
CCT GAG ATC TTC GGC AAA GCC TCT GAG TCC TTG		4342
TTT GGC ATT GAC GTG AAG GAA GCA GAC CCC ACC		4384
TAT GTC CTT GTC ACC TGC CTA GGT CTC TCC TAT		4426
CTG GGT GAT AAT CAG ATC ATG CCC AAG ACA GGC		4468
ATT GTC CTG GTC ATG ATT GCA ATG GAG GGC GGC		4510
GAG GAG GAA ATC TGG GAG GAG CTG AGT GTG ATG	GAG GTG TAT	4552

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GAT GGG AGG GAG CAC AGT GCC	TAT GGG GAG CCC AGG AAG CTG	4594
CTC ACC CAA GAT TTG GTG CAG	GAA AAG TAC CTG GAG TAC GGC	4636
AGG TGC CGG ACA GTG ATC CCG	CAC GCT ATG AGT TCC TGT GGG	4678
GTC CAA GGG CCC TCG CTG AAA	CCA GCT ATG TGA	4711
AAGTCCTTGA GTATGTGATC AAGGT	CAGTG CAAGAGTTC	4750
GCTTTTTCTT CCCATCCCTG CGTGA	AGCAG CTTTGAGAGA GGAGGAAGAG	4800
GGAGTCTGAG CATGAGTTGC AGCCA	AGGCC AGTGGGAGGG GGACTGGGCC	4850
AGTGCACCTT CCAGGGCCGC GTCCA	GCAGC TTCCCCTGCC TCGTGTGACA	4900
TGAGGCCCAT TCTTCACTCT GAAGA	GAGCG GTCAGTGTTC TCAGTAGTAG	4950
GTTTCTGTTC TATTGGGTGA CTTGG	AGATT TATCTTTGTT CTCTTTTGGA	5000
ATTGTTCAAA TGTTTTTTTT TAAGG	GATGG TTGAATGAAC TTCAGCATCC	5050
AAGTTTATGA ATGACAGCAG TCACA	CAGTT CTGTGTATAT AGTTTAAGGG	5100
TAAGAGTCTT GTGTTTTATT CAGAT	TGGGA AATCCATTCT ATTTTGTGAA	5150
TTGGGATAAT AACAGCAGTG GAATA	AGTAC TTAGAAATGT GAAAAATGAG	5200
CAGTAAAATA GATGAGATAA AGAAC	TAAAG AAATTAAGAG ATAGTCAATT	5250
CTTGCCTTAT ACCTCAGTCT ATTCT	GTAAA ATTTTTAAAG ATATATGCAT	5300
ACCTGGATTT CCTTGGCTTC TTTGA	GAATG TAAGAGAAAT TAAATCTGAA	5350
TAAAGAATTC TTCCTGTTCA CTGGC	TCTTT TCTTCTCCAT GCACTGAGCA	5400
TCTGCTTTTT GGAAGGCCCT GGGTT	AGTAG TGGAGATGCT AAGGTAAGCC	5450
AGACTCATAC CCACCCATAG GGTCG	TAGAG TCTAGGAGCT GCAGTCACGT	5500
AATCGAGGTG GCAAGATGTC CTCTA	AAGAT GTAGGGAAAA GTGAGAGAGG	5550
GGTGAGGGTG TGGGGCTCCG GGTGA	GAGTG GTGGAGTGTC AATGCCCTGA	5600
GCTGGGGCAT TTTGGGCTTT GGGAA	ACTGC AGTTCCTTCT GGGGGAGCTG	5650
ATTGTAATGA TCTTGGGTGG ATCC		5674

- (2) INFORMATION FOR SEQUENCE ID NO: 9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: singular (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-2 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCCATCCAGA	TCCCCATCCG	GGCAGAATCC	GGTTCCACCC	TTGCCGTGAA	50
CCCAGGGAAG	TCACGGGCCC	GGATGTGACG	CCACTGACTT	GCACATTGGA	100
GGTCAGAGGA	CAGCGAGATT	CTCGCCCTGA	GCAACGGCCT	GACGTCGGCG	150
GAGGGAAGCA	GGCGCAGGCT	CCGTGAGGAG	GCAAGGTAAG	ACGCCGAGGG	200
AGGACTGAGG	CGGGCCTCAC	CCCAGACAGA	GGGCCCCAA	TTAATCCAGC	250
GCTGCCTCTG	CTGCCGGGCC	TGGACCACCC	TGCAGGGGAA	GACTTCTCAG	300
GCTCAGTCGC	CACCACCTCA	CCCCGCCACC	CCCCGCCGCT	TTAACCGCAG	350
GGAACTCTGG	CGTAAGAGCT	TTGTGTGACC	AGGGCAGGGC	TGGTTAGAAG	400
TGCTCAGGGC	CCAGACTCAG	CCAGGAATCA	AGGTCAGGAC	CCCAAGAGGG	450
GACTGAGGGC	AACCCACCCC	CTACCCTCAC	TACCAATCCC	ATCCCCCAAC	500
ACCAACCCCA	CCCCCATCCC	TCAAACACCA	ACCCCACCCC	CAAACCCCAT	550
TCCCATCTCC	TCCCCCACCA	CCATCCTGGC	AGAATCCGGC	TTTGCCCCTG	600
CAATCAACCC	ACGGAAGCTC	CGGGAATGGC	GGCCAAGCAC	GCGGATCCTG	650
ACGTTCACAT	GTACGGCTAA	GGGAGGGAAG	GGGTTGGGTC	TCGTGAGTAT	700
GGCCTTTGGG	ATGCAGAGGA	AGGGCCCAGG	CCTCCTGGAA	GACAGTGGAG	750
TCCTTAGGGG	ACCCAGCATG	CCAGGACAGG	GGGCCCACTG	TACCCCTGTC	800
	CCACCTTTTC				850
	GGGGTTGGGG				900
AAGAGGGAGG	ACTGAGGGGA	CCTTGGAGTC	CAGATCAGTG	GCAACCTTGG	950
GCTGGGGGAT	CCTGGGCACA	GTGGCCGAAT	GTGCCCCGTG	CTCATTGCAC	1000
CTTCAGGGTG	ACAGAGAGTT	GAGGGCTGTG	GTCTGAGGGC	TGGGACTTCA	1050
GGTCAGCAGA	GGGAGGAATC	CCAGGATCTG	CCGGACCCAA	GGTGTGCCCC	1100
CTTCATGAGG	ACTCCCCATA	CCCCGGCCC	AGAAAGAAGG	GATGCCACAG	1150
AGTCTGGAAG	TAAATTGTTC	TTAGCTCTGG	GGGAACCTGA	TCAGGGATGG	1200
CCCTAAGTGA	CAATCTCATT	TGTACCACAG	GCAGGAGGTT	GGGGAACCCT	1250
	AGGTGTTGGT				1300
GGTTCCCCCT	TGAGAAAGGG	CAGTCCCTGG	CAGGAGTAAA	GATGAGTAAC	1350
	CCATCATAAC				1400
	CGTGGGGTAA				1450
	GGAGTTGATG				1500
	CTCTGGTCGA				1550
	AGAGCCTGAG				1600
GCAGCAAGGG	GGCCCCATAG	AAATCTGCCC	TGCCCCTGCG	GTTACTTCAG	1650
	CAGGGCTGTC				1700
	GAAGGGGAGG				1750
	GGTCTCAGGC				1800
	CCAGGACACC				1850
	GAGGACCTGG				1900
	TACCATATCA				1950
CAAGCCAGCA	AAAGGGTGGG	ATTAGGCCCT	ACAAGGAGAA	AGGTGAGGGC	2000

CCTGAGTGAG CACAGAGGGG ACCTTCCACC CAAGTAGAGT GGGAGTCTCA 2050 GCGAGTCTGC CAACCACCTGC TGAGACTTCT GGGAGTCTCCACC 2150 TCCAGGAACC AGGCAGAGC AGTCCAGCACC AGTCCAGCC 2200 AGACCAAGG GGCACCACCC CCCAAACAA ATGGGACTC AGGGGGCCTG 2300 GCCTCACCCC CCCACACCACC CCCACACCCAC AGGGGCCTC AGGGGCCTC 2300 GCCTCACCCC CCCACTCCCC CCCACACCCC AGGGCTCC AGGGGGCCCC 2400 AGGCTCACCC AGGCCTCCCC CCTGAGCATC TGAGGGGGCAC 2400 AGGCTGACAA ATGGGACCCCA AGGCACTCCA AGGCACTTCA AGGAGAAGAT 2450 AGGCTGACAA ATGCCTC CCTGAGCCTC AGGCCTCCA AGGCTCCCA AGGCTCCCC 2500 TAAGCCTC CTTGTCACCC AGGCCTCCA AGGCTCACCAC AGTCACAC AGTCACTC 2550 CCAGCTCCT CTCTGCTCCCC AGCCTCACACACACACACACACACACACACACACACACAC
GCAGTCTGCA CACTGAAGGC CCGTGCATTC CTCTCCCAGG AATCAGGAACC 2150 TCCAGGAACC AGGCAGTGAG GCCTTGGTCT GAGTCAGTGC 2250 AGACCAAGG GACAGCAGAC AGTGCCAACA ATGGACTTC GCCTGCACCCC CCCAGAACAA ATGGGACTC AGAGGGCCTG 2350 CCTCACCCT CCCTATTCTC AGTCTGCAG CTGAAGGTTC TGAGGGGCCC 2360 CTGTACCTA AGGTGCCCTC CCCACACCCC AGGCATCAA ATGGGACACC 2400 AGGCTCAAA ATGGACCCCAA AGGCATCAAA AGGAGAACAT 2450 CTGTAAGTAA AGTCTTCACAA AGGCTCCAAA AGTTCACCC 2500 TAAGGCCTCA CACACGCTCC CTGCCACACTC CCCTGACACAC AGTCATC 2550 CCCAGCTCCT CTCTCTCCC AGCCCTCAAA AGTCACAC AGTCACAC 2550 CCCAGCTCCT CTCTCTCCCC AGCCCTCAAA AGTCCACAC AGTCCACAC 2550 CCCAGCTCCT CTCTCTCTCCC CCCTGACCAC CTCTGCACAC AGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
TCCAGGANCC AGGCCAGAG ACTGCCACAC CGAGTCACT CGAGTCACAC 2250 AGAGCAGAGG GGCCCACCCG CCCAGAACAA ATGGGACTC AGAGGGCCTG 2250 CCCTCACCCT CCCTAGACCAA ATGGGACTC AGAGGGCCTG 2300 GCCTCACCCT CCCTATCCTC CTTCAGGTTC TGAGGGGCC 2350 CTGTACCCTG AGTGCACTCC CTGAGGATTC AGGGGGCCTC 2400 AGGCTGACAA GTAGGACCCG AGGCACTCGA GGAGCATTCA AGGAGAAGAT 2450 CTGTAAGTAA GCCTTGTCA GACCTCCAA AGGTCACTCC 2550 CTGAGCTCC CACACGCTCC TTCTCACC 2550 CTAAGGCCTCA CACACGCTCC CTTCACCCAA AGTCATC 2597 ATG CAC CACACGCTCAC CTGCACCACACCAA AGTCATCC 2500 ATG CAC CACACCACACACCAA AGCACACCAA AGCACCACCAA AGCACCACCAA AGCACCACCAACAACAACAACAACAACAACAACAACAACA
TCCAGGANCC AGGCCAGAG ACTGCCACAC CGAGTCACT CGAGTCACAC 2250 AGAGCAGAGG GGCCCACCCG CCCAGAACAA ATGGGACTC AGAGGGCCTG 2250 CCCTCACCCT CCCTAGACCAA ATGGGACTC AGAGGGCCTG 2300 GCCTCACCCT CCCTATCCTC CTTCAGGTTC TGAGGGGCC 2350 CTGTACCCTG AGTGCACTCC CTGAGGATTC AGGGGGCCTC 2400 AGGCTGACAA GTAGGACCCG AGGCACTCGA GGAGCATTCA AGGAGAAGAT 2450 CTGTAAGTAA GCCTTGTCA GACCTCCAA AGGTCACTCC 2550 CTGAGCTCC CACACGCTCC TTCTCACC 2550 CTAAGGCCTCA CACACGCTCC CTTCACCCAA AGTCATC 2597 ATG CAC CACACGCTCAC CTGCACCACACCAA AGTCATCC 2500 ATG CAC CACACCACACACCAA AGCACACCAA AGCACCACCAA AGCACCACCAA AGCACCACCAACAACAACAACAACAACAACAACAACAACA
AGAGCAGAGG GGACGACAGAC AGTGCCAACA CTGAAGGTTT GCCTGGAATG CACACCAAGG GCCCCACCCG CCCAGAACAA ATGGGACTCC AGAGGGCTG CACACCACCT CCCTATTCTC AGTCCTGCAG CCTGAGCATG TGCTGGCCGG CCCTCACCCT AGGTGCCCTC CCACTTCCTC CTCTCAGGTTC TGCAGGGGAC CTGTAACCCTG AGGTGCCCTC CCACTTCCTC CTCTCAGGTTC TGAGGGGGAC AGGCTGACAA GTAGGACCCG AGGCACTGGA GGAGCATTGA AGGAAGAT CTGTAAGTAA GCCTTTGTCA GAGCCTCCAA GGTCATCTC AGTTCTCACC CTGTAAGTAA GCCTTTGTCA GAGCCTCCAA GGTCATTGA AGGAAGAT CTGTAAGTAA GCCTTTGTCA GAGCCTCCAA GGTCACTGC CCCAGCTCCT GCCCGCACTC CTCCTCCTCC AGGCCTGTGG GTCTTCATTG CCCAGCTCCT GCCCGCACTC CTCCCTGCTC CCCTGACCAG AGTCATC AGT CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA 2639 GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GGC GGC GGC CAG GCT CCT GCT ACT GAG GAG CAG CAC CTG CAG ACC CT TCC TCT CTC CTT CTA CT CTA GTG GAA GTT ACC CTG GGG GAG GTG CCT GCT GCC CCCAC AGT CCT CTA CTA CTAC CAC AGT CCT CTA GAG GAA CCT CTAC ACC ACC ACC ACT CCT CAG GGA GCC CTC AGC CAC CCA CCC ACC ACC CAC AGT CCT CCT CAG GGA CCC TCC AGC CAC TCA CCC AGC AAC CAA AAG AGA GAG GGG CCA ATC AGT TCC ACC CAC CAC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATC GAT 2849 CCC GAC CTG GAG TCC CAA GAA GAG GAG GGG CCA AGA ATC GAT CAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATC GAT CAG GGC TCC AGC AAC CAA AAG GAA GAG GGG CCA AGC ATC AGT ACC ATC AAG AAT TGC CAG GAC TTC TTT CTC CTC CTC AAG TAT CCA CCC CAC CTG GAG TTC CTT TTT CTC CTC CTC AAG TAT CCA CCC CAC CTC GAG ACC CAC AAG GAA ATC CAG GTG GTG GTG AAA TTG CAG GCC CTC TTT TCC CTC CTC AAG TAT CCC CTC CAG TAC TTC CAC AGC CAC TTT TC CTC CTC AAG TAT CCC CTC CAG TAC TTC CAC AGC CAC TTT TC CTC CTC AAG TAT CCC CTC CAG TAC TTC CAC AGC CAC TTT TC CTC CTC AAG TAT CCC CTC CAG TAC TTC CAC CAC CTC CTG GAC AAA ATC CAC TTC CCC AAG ACA GGC CTC CTG AAA ATC CTT GTC CTC CAAG CAT TTC CAC CCC CTG GAG AAA ATC CTG GAG GAC CTC TCC TAC GAC CAC TTT TAC ATC TTT GCC ACC CTC GAG GAC CAT TTT CTC CCC ATC AGC CAC TTT TAC ATC CTC TTT GCC ACC CTC GAG GAG CAC ATT TTC GCA CAC CCC CTG GAC AAA ATC CTG GAG GAG CAC ATC TTC TTC GAC GAG GAC CTC TTT GAG GAG GAG GAC AAA ATC CTG GAG GAG GAC ATC T
CACACCAAGG GCCCCACCG CCCAGAACA ATGGGACTC AGAGGGCCTG GCCTCACCCT CCCTATTCTC AGTCCTGCAG CCTGAGCATG TGCTGGCCGG CTGTACCCTC AGGTGCCCTC CCCACTTCCTC CTTCAGGTTC TGAGGGGAC CTGTACCCTC AGGTGCCCTC CCACTTCCTC CTTCAGGTTC TGAGGGGAC CTGTAAGTAA GCCTTTGTCA GAGCCTCCAA GGAGCATTGA AGGAGAAGAT CTGTAAAGTAA GCCTTTGTCA GAGCCTCCAA GGTCCACTCGG CTAAGGCCTCA CACACGCTCC TTCTCTCCCCC AGGCCATTGA GTTCTCATTG CCACACGCTCCT GCCCGCACTC CTGCCTGCTG CCCTGACCAG AGTCATC CTT GAG GCC CTG GCC CAC CAC CAC CAC CAC CAC CAC CAC CA
GCCTCACCCT CCCTATTCTC AGTGCCCCC CCACTTCCCTC CTTCAGGCTC 2350 CTGTACCCTG AGGGCCCCCC CACTTCCCTC CTTCAGGTTC TGAGGGGGAC 2400 AGGCTCACAA GTAGGACCCG AGGCACTGGA GGAGCATTGA AGGAGAAGAT 2450 CTGTAAGTAA GCCTTGTCACC GGCCCCCCACCC CCCCAGCTCC CTCTCTCCC AGGCCTCCACCC 2500 TAAGGCCTCA CACCACCCCC CTCTCCCCC AGCCCTCTGC ACTCATCC 2550 CCCAGCTCCT CTCCCCCCC AGCCCCTG ACTCATCC 2557 ATG CCT CTT GAG GAG AGC CT GAG 2639 GCC CCT GAG GAG CAC ACC CT CCT GCC 2629 AGG CCT CCT AGC AGC ACC CTC CCT 2765 AGG CCT AGC AGC AGC ACC CCT CCT 2765 AGC TCT ACC AGC AG
CTGTACCCTG AGGTGCCCCC CACATTCCTC CTTCAGGTCC TAGGGGGAC 2450 AGGCTGACAA GTAGGACCCG AGGCACTGGA GGAGCATTGC 2500 TAAGGCCTCA CACACGCTCC TTCTCTCCCC AGGCCTGTGG GTCTTCATTG 2550 CCCAGCTCCT CTCCCTGCTG CCCTGACCAG AGTCTCATTG 2550 CCCAGCTCCT GCCCGCACTC CTGCCTGCTG CCCTGACCAG AGCAG AGA 2639 ATG CCT CTT GAG AGG AGC CTG GAG AGA 2639 GGC CTT GAG GAC CAC CTG GGC CGG 2681 CAG GCC CTG GGC CTG GGC CTG GGC 2681 CAG CCT GAG GAC CAC GAC CAC CAC 2622 2681 CTC CAG GAC CAC AGA AGC CAC CAC 2763 AGC CAC AGC AGC ACC
AGGCTGACAA GTAGGACCCG AGGCATCGA GGAGCATTGA AGGAGAAGAT CTGTAAGTAA GCCTTTGTCA GAGCCTCCAA GGTTCAGTTC AGTTCTACC 2500 TAAGGCCTCA CACACGCTCC TTCTCTCCCC AGGCCTGTGG GTCTTCATTG CCCAGCTCCT GCCCGCACTC CTGCCTGCTG CCCTGACCAG AGTCATC 2597 ATG CCT CTT GAG GAC AGG AGG AGT CAG CAC TGC AAG CCT GAA GAA 2639 GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG CCT GAT GAC ACC CTT GAG GAC AGG CAC TGC GGC CTG GTG GGT GCG CCT ACT CTA GTG GAA GTT ACC CTG GGC CTG GTG GCC CAC TAC CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC CTG GTG GCC ACT ACT CTA GTG GAA GTT ACC CTG GGG GAG GCC CTC CAG GCC TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CCA TCC AGC CAC CTG AGT CCT CCC CAC AGT CCT CCT CAG GGC CTC TCC GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATC GAT CCC GAC CTG GAG TCC GAG TTC CAA GCA GCA ATC AGT AGA AGG AGG GGC CTC GAG TCC GAG TTC CAA GCA GCA ATC AGA AGG AGG ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG AAG ACG AAG AAT TCC CAG GAC CAC AAA GAA AGG CAA ATC CTT AAG AAC CCC GCC AGA AAT CCC GAC ACA AAA GAA AAG GCA GAA ATC CTC CTC AAG AAAT TCC CAG GAC TTC TTT CTC CTC TCA AAG TAC CTC AGA AAT TCC CAG GAC TTC TTT CCC CTC AAG ACC CTC CCC CC AAC CCC ATC ACA AAA GCA GAA ATC CTT GAC AAC CTC AGA AAT TCC CAG GAC TTC TTT CCC CTC AAG ACC CTC CTC AGA AAT TCC CAG GAC TTC TTT CCC CTC AAG ACC CTC CTC AGA AAT TCC CAG GAC TTC TTT CCC CTC AAG ACC CTC CTC AGA AAT TCC CAG GAC TTC TTT CCC CTC AAG ACC CTC CTC AGA AAT TCC CAG GAC TTC TTT CCC CTC AAC ATC CAG GAC AAC ACC AGC CTC TCC TAC GAC GCC CTT GTT GCC CTC GAC GAC ATC CAG GCC CTC TCC TAC GAC CTC GTC GCC CTC GTC GAC GTC ATC AGA AAT TCC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG ATA GAG GCC CTC TCC TAC AAT ACC CTC CTC AAC AAC GCC AAA ACC AGC CTC CTG ATA ATC GTC CTC ATC ACC TGC CTG ATA GAG GCC CTC TCC TAC AAT ATC GCC CTC ATC ACC TTC ATC AAC ACC AGC TAT GTG AAA GTC CTG GCC CTG GAC AAT ACC CTG CATA ACC ACC ATC CTG GAG TAC CTG GCC CTG AAC AAT CAC ATT GAA ACC AGC TAT GTG AAA GTC CTG GCC CATA ACA CTA AAA ATC GAA ACC AGC TAT GTG AAA GTC CTG CCC CTG CATA ACA CTC AATC GAT ACC AGC TAT G
CTGTAAGTAA GCCTTTGTCA GAGCCTCCACAGGCCC 2500 TAAGGCCTCA CACACGCCCC TTCTCTCCCC AGGCCTGTGG GTCTTCATTG 2550 CCCAGCTCCT GCCGGCACTC CTGCTGCTG CCCTGACCA AGTCATC 2597 ATG CCT CTT GAG CAG AGC CCT GAA AGA 2639 GCC CTT GAG CAG CAG CAC TGC GAA AGA 2639 GCC CTT GAG GAG CAG CAC TGC GAG CCT CCT GCC 2681 CCT CCT <td< td=""></td<>
TAAGGCCTCA CACACGCTCC TTCTCTCCCC AGGCCTGAG 2550 CCCAGCTCCT GCCCGCACTC CTGCCTGCTG CCCTGACCAG AGTCATC 2597 ATG CCT CTG GAG CAG AGC CAC TGC AAG CAG AGC 2681 2639 GGC CTG GGC GGG 2681 CGC 2681 CGC 2681 CGC CCT GGC CCT GGC 2681 CCC 2765 GGC CCT GCC 2765 GCC CCT AGC ACA ACC GCT GCC 2765 GCC CCT AGC AGC AGC AGC CCT GCC 2765 GAG GCC CCT AGC AAG AGC CCT CCC AGC AGC AGC CCT CCC AGC AGC AGC CCT CCT CCT CAC AGC AGC AGC CCT CTC CAC AGC AGC CTC CAC
CCCAGCTCCT GCCCGCACTC CTGCCTGCTG CCCTGACCA AGTCATC 2597 ATG CCT CTT GAG CAG AGT CAG AGT CAG CAC TGC AAG CCT GAA GAA 2639 GGC CTT GAG GCC CGA GGA AGT CAG CAC CTG GTG GGT GGG 2681 CAG GCT CCT GCT ACT GAG GAG GCC CTG GGC CTG GTG GGT GCC 2765 GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC 2807 TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT 2849 GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATC GAT 2849 GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATC GAT 2849 GAG GGC TCC AGC AAC CAA GAA GAG GAG GAC ACA ATC AGT AGG AAG 2933 ATG GTT GAG TTC GAG TTC CAT TTT CTG CTC CTC AAG TAT CGA GAC 2975 AGG GAG CCG GTC ACA AAG GCA GAA ATC CAG GTG GTC CTC 3017 AGA AAT TGC CAG GAC TTC TTT CCC GTG AAC ATC AGC AGC GTC CTC 3017 AGA AAT TGC CAG GAC TTC TTT CTT TTT CTT GTC ATC AGC AAA GCC 3059 TCC GAG TAC TTG CAG CTG GTC TTT GTC GTG GAC AAT CAG GTG GTA 3101 AGG GTC CCC ATC AGC CAC TTG TAC ATC CTG GTC ATC AGC GAC ATA 3101 AGG GTC CCC ATC AGC CAC TTG TAC ATC CTG GGC AAC ATC CTG GAA 3101 AGG GTC CCC ATC AGC GAC TTC TTG GGG GAC AAT CAG GTG CTG 3143 AGA CAG GGC CTC CTG GAT AATC GTG
CCCAGCTCCT GCCCGCACTC CTGCCTGCTG CCCTGACCA AGTCATC 2597 ATG CCT CTT GAG CAG AGT CAG AGT CAG CAC TGC AAG CCT GAA GAA 2639 GGC CTT GAG GCC CGA GGA AGT CAG CAC CTG GTG GGT GGG 2681 CAG GCT CCT GCT ACT GAG GAG GCC CTG GGC CTG GTG GGT GCC 2765 GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC 2807 TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT 2849 GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATC GAT 2849 GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATC GAT 2849 GAG GGC TCC AGC AAC CAA GAA GAG GAG GAC ACA ATC AGT AGG AAG 2933 ATG GTT GAG TTC GAG TTC CAT TTT CTG CTC CTC AAG TAT CGA GAC 2975 AGG GAG CCG GTC ACA AAG GCA GAA ATC CAG GTG GTC CTC 3017 AGA AAT TGC CAG GAC TTC TTT CCC GTG AAC ATC AGC AGC GTC CTC 3017 AGA AAT TGC CAG GAC TTC TTT CTT TTT CTT GTC ATC AGC AAA GCC 3059 TCC GAG TAC TTG CAG CTG GTC TTT GTC GTG GAC AAT CAG GTG GTA 3101 AGG GTC CCC ATC AGC CAC TTG TAC ATC CTG GTC ATC AGC GAC ATA 3101 AGG GTC CCC ATC AGC CAC TTG TAC ATC CTG GGC AAC ATC CTG GAA 3101 AGG GTC CCC ATC AGC GAC TTC TTG GGG GAC AAT CAG GTG CTG 3143 AGA CAG GGC CTC CTG GAT AATC GTG
GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG 2681 CAG GCT CCT GCT ACT GAG GAG CAG CAG ACC GCT TCT TCC TCT 2723 TCT ACT CTA GTG GAA GTT ACC CTG GGG GAG GTG CCT GCT GCC 2765 GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC 2807 TCT CTG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT 2849 GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATC CGT TTT 2891 CCC GAC CTG GAG TCC GAG TTC CAA GCA GCA ATC ACT AGT AGG AGG GGC CCA AGA ATG TTT 2891 ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC 2975 AGG GAG CCG GTC ACA AAG GAA AG GAA ATG CTG GAG ACT ACT AGC AAG GAA ATG GTT CCTC 3017 AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC 3059 TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC TTC AGC AAA GCC 3059 TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC TTC AGC AAA GCC 3059 TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC TTC AGC AAA GCC 3059 TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC TTC AGC ATA GCC 3143 GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG 3143 GGC CTC TCC TAC GAT GGC CTG TTT GCC ATC TTC AGC ATA ATC GCA 3125 TCC AAG ACA GGC CTC CTG ATA ATC CTT GTC ACC TTG CTG GAG GAG 31269 CTG AGT ATG TTG GAG GTG TTT GAG GAG AAA ATC TTG GAG GAG 31269 CTG AGT ATG TTG GAG GTG TTT GAG GAG AAA ATC TTG GAG GAG 31269 CTG AGT ATG TTG GAG GTG TTT GAG GAG AAA ATC TTG GAG GAG 31269 CTG AGT ATG TTG GAG GTG TTT GAG GAG GAG G
GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG 2681 CAG GCT CCT GCT ACT GAG GAG CAG CAG ACC GCT TCT TCC TCT 2723 TCT ACT CTA GTG GAA GTT ACC CTG GGG GAG GTG CCT GCT GCC 2765 GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC 2807 TCT CTG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT 2849 GAG GGC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGA ATC CGT TTT 2891 CCC GAC CTG GAG TCC GAG TTC CAA GCA GCA ATC ACT AGT AGG AGG GGC CCA AGA ATG TTT 2891 ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC 2975 AGG GAG CCG GTC ACA AAG GAA AG GAA ATG CTG GAG ACT ACT AGC AAG GAA ATG GTT CCTC 3017 AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC 3059 TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC TTC AGC AAA GCC 3059 TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC TTC AGC AAA GCC 3059 TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC TTC AGC AAA GCC 3059 TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC TTC AGC ATA GCC 3143 GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG 3143 GGC CTC TCC TAC GAT GGC CTG TTT GCC ATC TTC AGC ATA ATC GCA 3125 TCC AAG ACA GGC CTC CTG ATA ATC CTT GTC ACC TTG CTG GAG GAG 31269 CTG AGT ATG TTG GAG GTG TTT GAG GAG AAA ATC TTG GAG GAG 31269 CTG AGT ATG TTG GAG GTG TTT GAG GAG AAA ATC TTG GAG GAG 31269 CTG AGT ATG TTG GAG GTG TTT GAG GAG AAA ATC TTG GAG GAG 31269 CTG AGT ATG TTG GAG GTG TTT GAG GAG GAG G
CAG GCT CCT GCT ACT GAG GAG CAG CAG ACC GCT TCT TCC CCT GAG GAG GCT GCT GCC 2765 GAC TCA CCG CCC CAC AGT CCT CAG 2807 TTC TCG ACC ATC AAC AAC AAC CAT CCT CTC AGC ABC 2849 GAG GCC ACC AAC CAA GAA GAG GCA CCAA CAA CAA CAA CAA CAA AAC CAA AGA GAG GCA ACA AAG AAA AAC CAA AGA GAG GCA AAA ATG CTA CTT CAA AAG GAA ATG CTA ATG CAC AAC AACA AAG CAA ATG CTC CAC ATG TTT CTC CAC ATG CTC CTC CTC<
TCT ACT CTA GTG GAA GTT ACC CTG GGG GAG GTG CCT GCT GCC GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT TCC TCG ACT ACC AAC CAA GAA GAG GAG GGG CCA AGA ATC TTT CAG GGC TCC AGC AAC CAA GAA GAG GAG GGA GGG CCA AGA ATG TTT CCC GAC CTG GAG TCC GAG TTC CAA GCA GCA ATC AGT AGG AAG ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC GAG AAT TGC CAG GAC TTC TTT TC CC GTG ATC TTC AGC AAA GCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTG GAA GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG AGA AAT TGC CAG GAC TTC TT GGC ATC GAG GTG GTG GAA GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG GAG GCC CTC TCC TAC GAC CTC GTG GAC AAT CAC GTG GTG GAA GCC CTC TCC TAC GAC CTC GTG GCC GAC AAT CAC TGC CTG ATA GAG GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA ATA GAG GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ACC TGG GAG ACA ACC TGC GAG GAG GAG GAG AAA ACC TCC AGG AAG CTG CTC ATG CAA GAT CTG GAC GAG AAA CTC CCC AGG AAG CTG CTC ATG GAG GAC ACT GTC AGA AAC TAC CCC AGG AAG CTG CTC ATG CAA GAT CTG GTG CAG AAA ACC TCC AGG AAG CTG CTC ATG CAA GAT CTG GTG CAG AAA ACC TCC ATT TCC TCT GAG GAG GAG GAC ACT GTT GAA ACC TAC CAC ATT TCC TCT GAC CAC AGG GCC CTC ATT GAA ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC CGT AGA GAA CCT CAC ATT TCC TCT CAC CAT ACA CTA AAG ATC GGT ATG GAA ACC TCC ATT TCC TCT CAC CAT ACA CTA AAG ATC GGT ATG GAA ACC TCC ATT TCC TCT GAC CAC CCC CTG GAG GAG ACCT CAC ATT TCC TCT CAC CAC CCC CTG TTGGATATGA ACC AGC TAT GTG AAA GAG TGA ACC TCC TCTCTTTG AAAAGAGAG TCAACACTTC TTAGGAGTATGA ACC TCC TTTCTTTA AACAAATGGTT CAACACTTC TTAGGAGTATGA ACC TCC TTTCTTTTA AACAAATGGTT CAACACTTC TTAGGAGTATGA ACCACCTTCC GGGCCCCATC CATTAGCTTC CACTAGCTCTC TTGGAACCTT TAGGAACTT CAGCATTCT ACCACCTTCCA GGGCCCCATC CATTAGCTTC CACTAGCTCTC TTGGAACCTT TAGGAACTT CAGCATTCTT ACCACCTTCTTTTAACAATTTAACACTTT TAGGATTAT AACTTTTCTTT ACCACCTTTTT
GAC TCA CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC 2807 TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT 2849 GAG GGC TCC AGC AAC CAA GAA GAG GGG GCG CCA AGA ATG TTT 2891 CCC GAC CTG GAG TCC GAG TTC CAA GCA GCA ATC AGT AGG AAG 2933 ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC 2975 AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGT GTC CTC 3017 AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC 3059 TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTG GAA 3101 GTG GTC CCC ATC AGC CAC ATG TAC ATC CTT GTC ACC TGC CTG 3143 GGC CTC TCC TAC GAC CAC TTG TAC ATC CTT GTC ACC TGC CTG 3143 GGC CTC TCC TAC GAC CCT GTG GGC GAC AAT CAG GTC ATG 3185 CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA 3227 ATA GAG GGC GAC TGT GCC CTG GAG GAG AAA ATC TGG GAG GAG 3269 CTG AGT ATG TTG GAG GTG TTT GAG GGG AGA GAG GAG
TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT 2849 GAG GGC TCC AGC AAC CAA GAA GAG GAG GAG GGG CCA AGA ATG TTT 2891 CCC GAC CTG GAG TCC GAG TTC CAA GCA GCA ATC AGT AGG AAG 2933 ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC 2975 AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGT GTC CTC 3017 AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC 3059 TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTG GAA 3101 GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG 3143 GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG 3185 GCC AAA ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA 3227 ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG 3226 CTG AGT ATG TTG GAG GTG TTT GAG GGG GAG GA
GAG GGC TCC AGC AAC CAA GAG GAG GGG CCA AGA ATG GAG TTT 2891 CCC GAC CTG GAG TCC GAG GCA AAG 2933 ATG GTT GAG GTT CTT CTC CTC AAG AAG 2975 AGG GAG CTG GTC CTC AAG AAT CGA GCC 2975 AGG GAG CTC AAG GAA ATG CTC GAG AGC AAG GAA ATG CTC CTC 3017 AGA AAT TGC CAG AAG GTC TTT CTC GAG AGC CTC 3017 AGA AAC TTG CAG CTC GTC GTC GTC GTC GTC TTT CTC GTG ATC TTC ACA ATC CTG ATC ATC
CCC GAC CTG GAG TCC GAG TTC CAA GCA GCA ATC AGT AGG AAG 2933 ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC 2975 AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGT GTC CTC 3017 AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC 3059 TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTG GAA 3101 GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG 3143 GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG 3185 CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA 3227 ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG 3269 CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAC AGT GTC 3311 TTC CAA CAT CCC AGG AAG CTG CTC ATG CAA GAT CTG GTG CAG 3353 GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC ATA GAT CCT 3353 GAA AAC TAC CTG GAG TAC CGG CAG GTG CCA AGG GCC CTC ATT GAA 3437 ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT 3479 GCA TAC GAG TTC CTG TAG CAC CAT ACA CTA AAG ATC GGT 3479 GGA GAA GAG TGA 3542 GTCTCACCA ATT TCC TAC CAC CAT ACA CTA AAG ATC GGT 3521 TTG AGA GAG GAA GAG TGA 3542 GCACCTTCCA GGGCCCATC CATGACTCT CACTGCTCT TTGGATATGA
ATG GTT GAG TTG GTT CAT TTT CTG CTC AAG GAC GCC 3975 AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GAC AGC 3017 AGA AAT TGC CAG GAC TTC TTT CCC GTC AAA GCC 3017 AGA AAT TGC CAG GAC TTT CCC GAG GAG GAG AAA GCC AAA GCC AAA GCC AAA 3101 GTC CCC ATC AGC CAC TTG GAC ATC CTTG AAC ACC TAG 3143 GGC CCC TAC GGC CTG CTG CTG GCC AAT CAG GTG 3143 GCC CTC AAC ACA ACA GGC AAT CAG AAT CAG
AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGT CTC 3017 AGA AAT TGC CAG GAC TTT CCC GTG ATC TTC AGC AAA GCC 3059 TCC GAG TAC CTG GTC TTT GCC ATC GAG GAG 3101 GTG GTC CCC ATC AGC CAC TTG TAC ATC CTG CTG GAG ATC CTG CTG GAG AAT CAG GTC ATG 3143 GCC CTC TAC GAC CTG CTG ATC CTG CTG CTG CTG CTG CTG CTG CTG ATA ATC GCA ATC GCA ATC GCA ATC GCA ATC GCA GAG ATC GCA ATC GCA GAG ATC
AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTA AAA GCC GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG GCC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG ATA GAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAC AGT GTC TTC GCA CAT CCC AGG AAG CTG CTC ATG CAA GAT CTG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT TTG AGA GAG CGA GAA GAG TGA GCACCTTCCA GAGGCCCATC CAGTAGCTC CAC CAT ACA CTA AAG ATC GGT GCACCTTCCA GGGCCCCATC CAGTAGCTTC CACTGCCTCG TGTGATATGA GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA 3642 GCCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA 3642 GTTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3792 GTTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CAGCACTCAA 3792 GTTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG
AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTA AAA GCC GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG GCC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG ATA GAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAC AGT GTC TTC GCA CAT CCC AGG AAG CTG CTC ATG CAA GAT CTG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT TTG AGA GAG CGA GAA GAG TGA GCACCTTCCA GAGGCCCATC CAGTAGCTC CAC CAT ACA CTA AAG ATC GGT GCACCTTCCA GGGCCCCATC CAGTAGCTTC CACTGCCTCG TGTGATATGA GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA 3642 GCCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA 3642 GTTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3792 GTTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CAGCACTCAA 3792 GTTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG
TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GAA GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG S185 CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAG GA
GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG 3143 GGC CTC TAC GGC CTG CTG GGC GAC ATG 3185 CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GAC AGC 3227 ATA GAG GGC CAC TGT GCC CCT GAG GAG AAA ATC GGA GAG GAG GAG 3269 CTG AGT TTG GAG GGG AGG GAG CTG CAG CAG GAG GAG GAG CTG CAG CTG CAG CTG ATT GAG GAG ATT
GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAG GA
CCC AAG ACA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAC GAC AGT GTC 3311 TTC GCA CAT CCC AGG AAG CTG CTC ATG CAA GAT CTG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT TTG AGA GAG GGA GAA GAG TGA GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA 3642 GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG 3792 GTTTATGAAT GTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG
ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG 3269 CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAG GA
CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAG GA
TTC GCA CAT CCC AGG AAG CTG CTC ATG CAA GAT CTG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT TTG AGA GAG GGA GAA GAG TGA GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3353 3427
GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT TTG AGA GAG GGA GAA GAG TGA GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3792 GTTTATGAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842
GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT TTG AGA GAG GGA GAA GAG TGA GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3792 GTTTATGAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792
GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT TTG AGA GAG GGA GAA GAG TGA GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3792 GTTTATGAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792
ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT TTG AGA GAG GGA GAA GAG TGA GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3742 TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842
GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT TTG AGA GAG GGA GAA GAG TGA GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3742 TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842
TTG AGA GAG GGA GAA GAG TGA GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3742 TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842
GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT 3592 GCACCTTCCA GGGCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA 3642 GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG 3692 TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3742 TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGACCTT CAGCATCCAA 3792 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842
GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA 3642 GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG 3692 TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3742 TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGACTT CAGCATCCAA 3792 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842
GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG 3692 TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3742 TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842
TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3742 TTGTTCAAAT GTTCCTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842
TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842
GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842
GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842
TAAGAGTCCT GTTTTTTATT CAGATTGGGA AATCCATTCC ATTTTGTGAG 3892
TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG 3942
TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT 4042
MAAMMAMMA 3.033 MAA333 3.033 MM333 MC-0110 MC-
TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT 4092
TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT 4092 TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC 4142 CCTGGTAGTA GTGGG 4157

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- (2) INFORMATION FOR SEQUENCE ID NO: 10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 662 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-21 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGATCCCCAT GGA	TCCAGGA AGAATCCAGT	TCCACCCCTG	CTGTGAACCC	50
AGGGAAGTCA CGG	GGCCGGA TGTGACGCCA	CTGACTTGCG	CGTTGGAGGT	100
CAGAGAACAG CGA	GATTCTC GCCCTGAGCA	ACGGCCTGAC	GTCGGCGGAG	150
GGAAGCAGGC GCA	GGCTCCG TGAGGAGGCA	AGGTAAGATG	CCGAGGGAGG	200
ACTGAGGCGG GCC	TCACCCC AGACAGAGGG	CCCCCAATAA	TCCAGCGCTG	250
CCTCTGCTGC CAG	GCCTGGA CCACCCTGCA	GGGGAAGACT	TCTCAGGCTC	300
AGTCGCCACC ACC	TCACCCC GCCACCCCC	GCCGCTTTAA	CCGCAGGGAA	350
CTCTGGTGTA AGA	GCTTTGT GTGACCAGGG	CAGGGCTGGT	TAGAAGTGCT	400
CAGGGCCCAG ACT	CAGCCAG GAATCAAGGT	CAGGACCCCA	AGAGGGGACT	450
GAGGGTAACC CCC	CCGCACC CCCACCACCA	TTCCCATCCC	CCAACACCAA	500
CCCCACCCC ATC	CCCCAAC ACCAAACCCA	CCACCATCGC	TCAAACATCA	550
ACGGCACCCC CAA	ACCCCGA TTCCCATCCC	CACCCATCCT	GGCAGAATCG	600
GAGCTTTGCC CCT	GCAATCA ACCCACGGAA	GCTCCGGGAA	TGGCGGCCAA	650
GCACGCGGAT CC				662

INFORMATION FOR SEQUENCE ID NO: 11: (2)

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1640 base pairs
- (B) TYPE: nucleic acid (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (ix) FEATURE:
 - (A) NAME/KEY: cDNA MAGE-3
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCCGCGAGGG AAGCCGGCCC AG	GCTCGGTG AGGAGGCAAG	GTTCTGAGGG	50
GACAGGCTGA CCTGGAGGAC CA			100
AGATCTGCCA GTGGGTCTCC AT			150
GTTGCCCTGA CCAGAGTCAT C			171
ATG CCT CTT GAG CAG AGG	AGT CAG CAC TGC AAG	CCT GAA GAA	213
GGC CTT GAG GCC CGA GGA	GAG GCC CTG GGC CTG	GTG GGT GCG	255
CAG GCT CCT GCT ACT GAG			297
TCT ACT CTA GTT GAA GTC	ACC CTG GGG GAG GTG	CCT GCT GCC	339
GAG TCA CCA GAT CCT CCC	CAG AGT CCT CAG GGA	GCC TCC AGC	381
CTC CCC ACT ACC ATG AAC			423
GAG GAC TCC AGC AAC CAA			465
CCT GAC CTG GAG TCC GAG	TTC CAA GCA GCA CTC	AGT AGG AAG	507
GTG GCC GAG TTG GTT CAT	TTT CTG CTC CTC AAG	TAT CGA GCC	549
AGG GAG CCG GTC ACA AAG			591
GGA AAT TGG CAG TAT TTC	TTT CCT GTG ATC TTC	AGC AAA GCT	633
TCC AGT TCC TTG CAG CTG	GTC TTT GGC ATC GAG	CTG ATG GAA	675
GTG GAC CCC ATC GGC CAC	TTG TAC ATC TTT GCC	ACC TGC CTG	717
GGC CTC TCC TAC GAT GGC			759
CCC AAG GCA GGC CTC CTG	ATA ATC GTC CTG GCC	ATA ATC GCA	801
AGA GAG GGC GAC TGT GCC	CCT GAG GAG AAA ATC	TGG GAG GAG	843
CTG AGT GTG TTA GAG GTG	TTT GAG GGG AGG GAA	GAC AGT ATG	885
TTG GGG GAT CCC AAG AAG			927
GAA AAC TAC CTG GAG TAC			969
GCA TGT TAT GAA TTC CTG			1011
ACC AGC TAT GTG AAA GTC	CTG CAC CAT ATG GTA	AAG ATC AGT	1053
GGA GGA CCT CAC ATT TCC	TAC CCA CCC CTG CAT	GAG TGG GTT	1095
TTG AGA GAG GGG GAA GAG '	TGA		1116
GTCTGAGCAC GAGTTGCAGC CA	GGGCCAGT GGGAGGGGGT	CTGGGCCAGT	1166
GCACCTTCCG GGGCCGCATC CC	TTAGTTTC CACTGCCTCC	TGTGACGTGA	1216
GGCCCATTCT TCACTCTTTG AAG			1266
TTTCTGTTCT GTTGGATGAC TT			1316
TTGTTCAAAT GTTCCTTTTA AC	GGATGGTT GAATGAGCGT	CAGCATCCAG	1366
GTTTATGAAT GACAGTAGTC AC	ACATAGTG CTGTTTATAT	AGTTTAGGAG	1416
TAAGAGTCTT GttTTTTACT CA			1466
TTGTGACATA ATAATAGCAG TG	GTAAAAGT ATTTGCTTAA	AATTGTGAGC	1516
GAATTAGCAA TAACATACAT GA	GATAACTC AAGAAATCAA	AAGATAGTTG	1566
ATTCTTGCCT TGTACCTCAA TC		AAATATGCAA	1616
ACCAGGATTT CCTTGACTTC TT	TG		1640

- (2) INFORMATION FOR SEQUENCE ID NO: 12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 943 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-31 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGATCCTCCA CCCCAGTAGA GTGGGGACCT CACAGAGTCT GGCCAACCCT	50
CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG	100
GCCCGTGGAT TCCTCTCCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG	150
AGGACTTGGT CTGAGGCAGT GTCCTCAGGT CACAGAGTAG AGGGGGCTCA	200
GATAGTGCCA ACGGTGAAGG TTTGCCTTGG ATTCAAACCA AGGGCCCCAC	250
CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT	300
TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC	350
CTCTCACTTC CTCCTTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGACC	400
AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTTG	450
TTAGAGCCTC CAAGGTTCCA TTCAGTACTC AGCTGAGGTC TCTCACATGC	500
TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCCAGCT CCTGCCCACA	550
CTCCCGCCTG TTGCCCTGAC CAGAGTCATC	580
ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA	622
GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG	664
CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCT	706
TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCC	748
GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC	790
CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT	832
GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC	874
CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG	916
GTG GCC AAG TTG GTT CAT TTT CTG CTC	943

- INFORMATION FOR SEQUENCE ID NO: 13: (2)
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1067 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (ix) FEATURE:
 - (A) NAME/KEY: cDNA MAGE-4
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

	GGG	CCA	AGC	ACC	TCG	CCT	GAC	GCA	GAG	TCC	TTG	TTC	CGA	39
GAA	GCA	CTC	AGT	AAC	AAG	GTG	GAT	GAG	TTG	GCT	CAT	TTT	CTG	81
CTC	CGC	AAG	TAT	CGA	GCC	AAG	GAG	CTG	GTC	ACA	AAG	GCA	GAA	123
ATG	CTG	GAG	AGA	GTC	ATC	AAA	AAT	TAC	AAG	CGC	TGC	TTT	CCT	165
GTG	ATC	TTC	GGC	AAA	GCC	TCC	GAG	TCC	CTG	AAG	ATG	ATC	TTT	207
GGC	ATT	GAC	GTG	AAG	GAA	GTG	GAC	CCC	GCC	AGC	AAC	ACC	TAC	249
ACC	CTT	GTC	ACC	TGC	CTG	GGC	CTT	TCC	TAT	GAT	GGC	CTG	CTG	291
			CAG									ATA		333
GTC	CTG	GGC	ACA	ATT	GCA	ATG	GAG	GGC	GAC	AGC	GCC	TCT	GAG	375
GAG	GAA	ATC	TGG	GAG	GAG	CTG	GGT	GTG	ATG	GGG	GTG	TAT	GAT	417
GGG	AGG	GAG	CAC	ACT	GTC	TAT	GGG	GAG	CCC	AGG	AAA	CTG	CTC	459
			TGG											501
GTA	CCC	GGC	AGT	AAT	CCT	GCG	CGC	TAT	GAG	TTC	CTG	TGG	GGT	543
			CTG											585
			AGG											627
			GAA											669
			rtgc <i>i</i>											719
TGC	ATCT	AAC A	AGCC	CTGT	SC AC	CAG	CTTC	CTI	rgcci	CGT	GTA	ACAT	GAG	769
GCCC	CATTO	CTT (CACTO	CTGT	rt G?	\AGA/	AAATA	A GTO	CAGT	TTC	TTA	GTAG:	rgg	819
GTTI	CTAT	TTT	rgtt	GAT	SA C	rtgg?	AGATI	TAT	rctc:	rgtt	TCC	rttt?	ACA	869
			rgttc									CAT	CCA	919
AGTI	TAT	SAA T	rcgt <i>i</i>	\GTT!	AA CC	TAT	ATTGO	C TGT	raati	ATAT	GTT	ragg <i>i</i>	AGT	969
	AGTCI		rttti											1019
TTGO	GAC	ATA A	ATAAC	CAGC	AG TO	GAG	FAAG 1	TA T	CTAG	AAGT	GTG	AATTO	2	1067

(2)	INFORMATION FOR SEQUENCE ID NO: 14:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 226 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: singular
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: genomic DNA
	(ix) FEATURE:
	(A) NAME/KEY: MAGE-5 gene
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG ATCTGTAAGT	50
AAGCCTTTGT TAGAGCCTCC AAGGTTCAGT TTTTAGCTGA GGCTTCTCAC	100
ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC AGCTCCTGCC	150
CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC	184
ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA	226

(2)	INFORMATION FOR SEQUENCE ID NO: 15:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 225 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: singular
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: cDNA
	(ix) FEATURE:
	(A) NAME/KEY: MAGE-6 gene
	(xi) SEOUENCE DESCRIPTION: SEO ID NO: 15:

TAT	TTC	TTT	CCT	GTG	ATC	TTC	AGC	AAA	GCT	TCC	GAT	TCC	TTG	42
CAG	CTG	GTC	TTT	GGC	ATC	GAG	CTG	ATG	GAA	GTG	GAC	CCC	ATC	84
GGC	CAC	GTG	TAC	ATC	TTT	GCC	ACC	TGC	CTG	GGC	CTC	TCC	TAC	126
GAT	GGC	CTG	CTG	GGT	GAC	AAT	CAG	ATC	ATG	CCC	AGG	ACA	GGC	168
TTC	CTG	ATA	ATC	ATC	CTG	GCC	ATA	ATC	GCA	AGA	GAG	GGC	GAC	210
TGT	GCC	CCT	GAG	GAG										225

(2)	INFORMATION FOR SEQUENCE ID NO: 16:
(2)	
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 166 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: singular
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: genomic DNA
	(ix) FEATURE:
	(A) NAME/KEY: MAGE-7 gene
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

ACA	AGC	ACT	AGT	TTC	CTT	GTG	ATC	TAT	GGC	AAA	GCC	TCA	GAG	42
TGC	ATG	CAG	GTG	ATG	TTT	GGC	ATT	GAC	ATG	AAG	GAA	GTG	GAC	84
CCC	GCG	GCC	ACT	CCT	ACG	TCT	TGT	ACC	TGC	TTG	GGC	CTC	TCC	126
TAC	AAT	GGC	CTG	CTG	GGT	GAT	GAT	CAG	AGC	ATG	CCC	GAG	A	166

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